

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2005, 20:21:17 ; Search time 88.0482 Seconds
(without alignments)
483.186 Million cell updates/sec

Title: US-09-723-752b-115
Sequence score: 575

Sequence: 1 DIQLTQSPSLASVGDRLT.....YSTVPWTFGGSTKVEIKRTV 110

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	575	100.0	110	2	AAW70677 Anti-VEGF
2	575	100.0	110	2	AAW70687 Anti-VEGF
3	575	100.0	110	3	AAW70687 Anti-VEGF
4	575	100.0	110	3	AAW70687 Anti-VEGF
5	575	100.0	110	3	AAW70687 Anti-VEGF
6	575	100.0	110	3	AAW70687 Anti-VEGF
7	575	100.0	110	3	AAW70687 Anti-VEGF
8	575	100.0	110	3	AAW70687 Anti-VEGF
9	575	100.0	110	3	AAW70687 Anti-VEGF
10	575	100.0	110	3	AAW70687 Anti-VEGF
11	575	100.0	110	3	AAW70687 Anti-VEGF
12	575	100.0	110	3	AAW70687 Anti-VEGF
13	575	100.0	110	3	AAW70687 Anti-VEGF
14	575	100.0	110	3	AAW70687 Anti-VEGF
15	575	100.0	110	3	AAW70687 Anti-VEGF
16	575	100.0	110	3	AAW70687 Anti-VEGF
17	575	100.0	110	3	AAW70687 Anti-VEGF
18	575	100.0	110	3	AAW70687 Anti-VEGF
19	575	100.0	110	3	AAW70687 Anti-VEGF
20	575	100.0	110	3	AAW70687 Anti-VEGF
21	575	100.0	110	3	AAW70687 Anti-VEGF
22	575	100.0	110	3	AAW70687 Anti-VEGF
23	575	100.0	110	3	AAW70687 Anti-VEGF
24	575	100.0	110	3	AAW70687 Anti-VEGF
25	575	100.0	110	3	AAW70687 Anti-VEGF

25	566	98.4	108	8	ADG31770	ADG31770 V(L) doma
27	564	98.1	108	5	AAW70618	AAW70618 Anti-VEGF
28	564	98.1	108	5	ABP61187	ABP61187 Humanised
29	564	98.1	108	8	ADG31782	ADG31782 V(L) doma
30	564	98.1	108	8	ADG31768	ADG31768 V(L) doma
31	564	98.1	108	8	ADG31893	ADG31893 V(L) doma
32	561	97.6	108	5	AAW70696	AAW70696 Anti-VEGF
33	561	97.6	108	5	ABP61265	ABP61265 Humanised
34	558	97.0	114	7	ADG26157	ADG26157 Anti-VEGF
35	557	96.9	114	7	ADG26156	ADG26156 Anti-VEGF
36	556	96.7	107	2	AAW68804	AAW68804 Variable
37	556	96.7	107	2	AAW70623	AAW70623 Humanised
38	556	96.7	107	5	AAW61192	AAW61192 Humanised
39	556	96.7	110	2	AAW70681	AAW70681 Anti-VEGF
40	556	96.7	110	2	AAW70683	AAW70683 Anti-VEGF
41	556	96.7	110	2	AAW70679	AAW70679 Anti-VEGF
42	556	96.7	110	3	AAW70685	AAW70685 Anti-VEGF
43	556	96.7	110	3	AAW70686	AAW70686 Anti-VEGF
44	556	96.7	110	3	AAW70687	AAW70687 Anti-VEGF
45	556	96.7	110	3	AAW70688	AAW70688 Anti-VEGF

ALIGNMENTS

RESULT 1
AAW70677 standard; peptide; 110 AA.

AAW70677;

27-JAN-1999 (first entry)

Anti-VEGF humanised antibody variable light domain of variant Y0101.

Light variable domain; murine; humanised antibody;

anti-vascular endothelial growth factor antibody; anti-VEGF antibody;

VEGF-induced angiogenesis; tumour; retinal disorder;

age-related macular degeneration; diabetic retinopathy;

rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

Synthetic.

Mus sp.

Homo sapiens.

MO9845331-A2.

15-OCT-1998.

03-APR-1998; 98WO-US006604.

07-APR-1997; 97US-00833504.

06-AUG-1997; 97US-00908469.

(GETH) GENENTECH INC.

Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

WPI, 1998-568337/48.

New humanised antibody with affinity for vascular endothelial growth

factor - for treatment of tumours, retinal disease and other angiogenic

states, also related nucleic acid, vectors and transformed cells.

Example 3, Fig 9A; 100pp; English.

The present sequence represents a variable light domain of an affinity-

matured anti-vascular endothelial growth factor (anti-VEGF) antibody

variant. The sequence is used in the course of the invention to produce

the humanised anti-VEGF antibody of the invention. The humanised

antibodies are used to inhibit VEGF-induced angiogenesis, particularly

for treating or preventing tumours (of any type) and retinal disorders

(e.g. age-related macular degeneration or diabetic retinopathy). They can

CC also be used to treat other conditions that involve angiogenesis, e.g.
 CC rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc
 XX
 SQ Sequence 110 AA;

Query Match 100.0%; Score 575; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 5.4e-34;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTSPSSLSASVGDRTTITCSASQDISNLYMWYQKPKAPKVLITFTSLHSGVPS 60
 DB 1 DIQLTSPSSLSASVGDRTTITCSASQDISNLYMWYQKPKAPKVLITFTSLHSGVPS 60
 QY 61 RFGSGSGTDFLTITSLQPEDPATYCCQYSTVPMPTFGGTVKIKRTV 110
 DB 61 RFGSGSGTDFLTITSLQPEDPATYCCQYSTVPMPTFGGTVKIKRTV 110

RESULT 2
 AAU70687
 ID AAU70687 standard; peptide; 110 AA.

AC AAU70687;
 XX
 DT 27-JAN-1999 (first entry)
 XX
 DE Anti-VEGF humanised antibody variable light domain of variant Y0317.

XX Light variable domain; murine; humanised antibody;
 XX anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
 XX VEGF-induced angiogenesis; tumour; retinal disorder;
 XX age-related macular degeneration; diabetic retinopathy;
 XX rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.

XX MO9845331-A2.

XX 15-OCT-1998.

XX 03-APR-1998; 98WO-US006604.

XX 07-APR-1997; 97US-00833504.

XX 06-AUG-1997; 97US-00908469.

XX (GETH) GENENTECH INC.

XX Bace M, Wells JA, Presta LG, Lowman HB, Chen YM;
 XX WPI; 1998-568337/48.

XX New humanised antibody with affinity for vascular endothelial growth
 XX factor - for treatment of tumours, retinal disease and other angiogenic
 XX states, also related nucleic acid, vectors and transformed cells.

XX Claim 27; Fig 10A; 100pp; English.

XX The present sequence represents a variable light domain of an affinity-
 CC matured anti-vascular endothelial growth factor (anti-VEGF) antibody
 CC variant. The sequence is used in the course of the invention to produce
 CC the humanised anti-VEGF antibody of the invention. The humanised
 CC antibodies are used to inhibit VEGF-induced angiogenesis, particularly
 CC for treating or preventing tumours (of any type) and retinal disorders
 CC (e.g. age-related macular degeneration or diabetic retinopathy). They can
 CC also be used to treat other conditions that involve angiogenesis, e.g.
 CC rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc

XX Sequence 110 AA;

Query Match 100.0%; Score 575; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 5.4e-34;

Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTSPSSLSASVGDRTTITCSASQDISNLYMWYQKPKAPKVLITFTSLHSGVPS 60
 DB 1 DIQLTSPSSLSASVGDRTTITCSASQDISNLYMWYQKPKAPKVLITFTSLHSGVPS 60
 QY 61 RFGSGSGTDFLTITSLQPEDPATYCCQYSTVPMPTFGGTVKIKRTV 110
 DB 61 RFGSGSGTDFLTITSLQPEDPATYCCQYSTVPMPTFGGTVKIKRTV 110

RESULT 3
 AAB13380
 ID AAB13380 standard; protein; 110 AA.

AC AAB13380;
 XX
 DT 21-NOV-2000 (first entry)
 XX

DE Anti-VEGF antibody Y0317 light chain variable domain.

XX Y0317; vascular endothelial cell growth factor; VEGF; antibody;
 XX antiinflammatory; cerebroprotective; cytostatic; antirheumatic;
 XX antiarthritic; antipsoriatic; antiarteriosclerotic; antidiabetic;
 XX antithyroid; excessive neovascularisation; tumour; rheumatoid arthritis;
 XX psoriasis; atherosclerosis; diabetes; retrolental fibroplasia;
 XX neovascular glaucoma; haemangioma; thyroid hyperplasia; Grave's disease;
 XX tissue transplantation; inflammation; oedema; trauma;
 XX complementarity determining region; CDR.

OS Unidentified.

XX Key Location/Qualifiers
 XX Region 24..33
 XX /label= CDR-L1
 XX Region 50..56
 XX /label= CDR-L2
 XX Region 69..97
 XX /label= CDR-L3

XX MO200037502-A2.

XX 29-JUN-2000.

XX 09-DEC-1999; 99WO-US029475.

XX 22-DEC-1998; 98US-00218481.

XX (GETH) GENENTECH INC.

XX Van Bruggen N, Ferrara N;
 XX WPI; 2000-442646/38.

XX Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis,
 XX diabetes and chronic inflammation in a mammal, comprises administering a
 XX human vascular endothelial cell growth factor antagonist.

XX Disclosure; Fig 14A; 60pp; English.

XX The present sequence is the light chain variable region of the affinity
 CC matured anti-vascular endothelial cell growth factor (anti-VEGF) antibody
 CC Y0317. Humanised F(ab)-12 and affinity matured anti-VEGF antibodies may
 CC be used to treat conditions characterised by undesirable excessive
 CC neovascularisation. Such conditions include tumours (especially solid
 CC ones), rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and
 CC other retinopathies, retrolental fibroplasia, age-related macular
 CC degeneration, neovascular glaucoma, haemangiomas, thyroid hyperplasias
 CC (including Grave's disease), corneal and other tissue transplantation,
 CC and chronic inflammation. Oedemas associated with tumours, strokes and
 CC head trauma, and ascites associated with malignancies, meigs's syndrome,
 CC lung inflammation, nephrotic syndrome, pericardial effusion and pleural
 CC effusion, may also be treated. Monoclonal antibodies are generated in

CC hybridoma cells and those with affinity for VEGF are identified by
CC immunoprecipitation or by an in vitro binding assay

XX Sequence 110 AA;

Query Match 100.0%; Score 575; DB 3; Length 110;
Best Local Similarity 100.0%; Pred. No. 5.4e-34;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSLASVGDRTVITTSASQDISNLYMWYQKRGKAPKVLIVFTSSLSHGVPS 60
DB 1 DIQLTQSPSLASVGDRTVITTSASQDISNLYMWYQKRGKAPKVLIVFTSSLSHGVPS 60

QY 61 RFGSGSGTDFLTITSLQPEDPATYCCOYSTVPMTFGQGTVEIKRTV 110
DB 61 RFGSGSGTDFLTITSLQPEDPATYCCOYSTVPMTFGQGTVEIKRTV 110

RESULT 4

ABP61256
ID ABP61256 standard; protein; 110 AA.

AC ABP61256;
DT 20-SEP-2002 (first entry)

DE Humanised anti-VEGF Y0317 antibody variable light domain.

XX Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
KM retinal disorder; intraocular neovascular disorder; Y0317; light chain;
KW variable domain.

OS Homo sapiens.
OS Mus sp.
OS Synthetic.

XX Location/Qualifiers

FT Domain 24..34
FT /label= CDR-L1
FT 50..56
FT /label= CDR-L2
FT 89..97
FT /label= CDR-L3

XX US2002032315-A1.

XX 14-MAR-2002.

XX 06-APR-1998; 98US-00056160.

XX 06-AUG-1997; 97US-0054856P.

XX (BACA/) BACA M.
PA (WELLS/) WELLS J A.
PA (PREST/) PRESTA L G.
PA (LOWM/) LOWMAN H B.
PA (CHEN/) CHEN Y M.

XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX WPI, 2002-517920/55.

PT New humanized anti-VEGF (vascular endothelial growth factor) antibodies
PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
PT mammal, particularly for treating tumor or retinal disorders.

PS Claim 27; Fig 10; 47pp; English.

XX The present invention relates to humanised anti-VEGF (vascular
CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),

CC particularly those having a tumour or a retinal disorder e.g. intraocular
CC neovascular disorders. The present sequence is an exemplary light chain
CC variable domain of the humanised anti-VEGF antibody of the invention

XX Sequence 110 AA;

Query Match 100.0%; Score 575; DB 5; Length 110;
Best Local Similarity 100.0%; Pred. No. 5.4e-34;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSLASVGDRTVITTSASQDISNLYMWYQKRGKAPKVLIVFTSSLSHGVPS 60
DB 1 DIQLTQSPSLASVGDRTVITTSASQDISNLYMWYQKRGKAPKVLIVFTSSLSHGVPS 60

QY 61 RFGSGSGTDFLTITSLQPEDPATYCCOYSTVPMTFGQGTVEIKRTV 110
DB 61 RFGSGSGTDFLTITSLQPEDPATYCCOYSTVPMTFGQGTVEIKRTV 110

RESULT 5

ABP61246
ID ABP61246 standard; protein; 110 AA.

AC ABP61246;
DT 20-SEP-2002 (first entry)

DE Humanised anti-VEGF Y0101 antibody variable light domain.

XX Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
KM retinal disorder; intraocular neovascular disorder; Y0101; light chain;
KW variable domain.

OS Homo sapiens.
OS Mus sp.
OS Synthetic.

XX Location/Qualifiers

FT Domain 24..34
FT /label= CDR-L1
FT 50..57
FT /label= CDR-L2
FT 89..97
FT /label= CDR-L3

XX US2002032315-A1.

XX 14-MAR-2002.

XX 06-APR-1998; 98US-00056160.

XX 06-AUG-1997; 97US-0054856P.

XX (BACA/) BACA M.
PA (WELLS/) WELLS J A.
PA (PREST/) PRESTA L G.
PA (LOWM/) LOWMAN H B.
PA (CHEN/) CHEN Y M.

XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX WPI, 2002-517920/55.

PT New humanized anti-VEGF (vascular endothelial growth factor) antibodies
PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
PT mammal, particularly for treating tumor or retinal disorders.

PS Example 3; Fig 9; 47pp; English.

XX The present invention relates to humanised anti-VEGF (vascular
CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for

CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
 CC particularly those having a tumor or a retinal disorder e.g. intracocular
 CC neovascular disorders. The present sequence is an exemplary light chain
 CC variable domain of the humanised anti-VEGF antibody of the invention
 SQ
 Sequence 110 AA;

Query Match 100.0%; Score 575; DB 5; Length 110;
 Best Local Similarity 100.0%; Pred. No. 5, 4e-34;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCSASODISNTLNTYQKRGKAPKLYIFTSSLHSGVPS 60
 DB 1 DIQLTQSPSSLSASVGDRTVITCSASODISNTLNTYQKRGKAPKLYIFTSSLHSGVPS 60
 QY 61 RFGSGSGTDFLTITSSLOPEDPATYCCQYSTVPTWTFGGTKVEIKRTV 110
 DB 61 RFGSGSGTDFLTITSSLOPEDPATYCCQYSTVPTWTFGGTKVEIKRTV 110

RESULT 6
 ADC26154
 ID ADC26154 standard; protein; 214 AA.

AC ADC26154;
 DT 18-DEC-2003 (first entry)
 DE Parent anti-VEGF Y0101 antibody wild-type light chain protein.

KM antibody variant; cytosstatic; cancer; parent; anti-VEGF;
 KM vascular endothelial growth factor; Y0101; light chain; wild-type.

OS Unidentified.
 OS WO2003068801-A2.

PN 21-AUG-2003.

PF 11-FEB-2003; 2003WO-US004184.

PR 11-FEB-2002; 2002US-0355895P.

PR 10-SEP-2002; 2002US-0409685P.

PA (GETH) GENENTECH INC.

PI Lowman HB, Marvin JS;

DR WPI; 2003-697521/66.

PT Making an antibody variant of a parent antibody specific to an antigen by
 PT identifying a target amino acid residue within the variable domain of the
 PT parent antibody and substituting the target residue with a different
 PT amino acid residue.

PS Example 1; SEQ ID NO 1; 81pp; English.

CC The invention relates to a novel method for making an antibody variant of
 CC a parent antibody specific to an antigen. This is achieved via
 CC identifying a target amino acid residue within the variable domain of the
 CC parent antibody and substituting the target residue with a different
 CC replacement amino acid residue such that the charge complementarity
 CC between the antibody and antigen is increased. The antibody variant of
 CC the invention demonstrates cytosstatic activity whilst the method may be
 CC useful for treating cancer. The current sequence is that of the parent
 CC anti-VEGF (vascular endothelial growth factor) Y0101 antibody wild-type
 CC light chain protein of the invention.

XX Sequence 214 AA;

Query Match 100.0%; Score 575; DB 7; Length 214;
 Best Local Similarity 100.0%; Pred. No. 9, 7e-34;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCSASODISNTLNTYQKRGKAPKLYIFTSSLHSGVPS 60
 DB 1 DIQLTQSPSSLSASVGDRTVITCSASODISNTLNTYQKRGKAPKLYIFTSSLHSGVPS 60

QY 61 RFGSGSGTDFLTITSSLOPEDPATYCCQYSTVPTWTFGGTKVEIKRTV 110
 DB 61 RFGSGSGTDFLTITSSLOPEDPATYCCQYSTVPTWTFGGTKVEIKRTV 110

RESULT 7
 ABB81107
 ID ABB81107 standard; protein; 237 AA.

AC ABB81107;
 DT 05-NOV-2002 (first entry)
 DE Anti-VEGF light chain fragment.

KM Immunoglobulin; promoter; cytosstatic; antiinflammatory; immunomodulator;
 KM neuroprotective; CD11; tissue factor; vascular endothelial growth factor;
 KM VEGF.

OS Synthetic.

Key Location/Qualifiers

FT Peptide 1..23
 FT /note="STII signal sequence TIR-1"

FT Protein 24..237
 FT /note="anti-VEGF light chain"

PN WO200261090-A2.

PD 08-AUG-2002.

PF 13-DEC-2001; 2001WO-US048691.

PR 14-DEC-2000; 2000US-0256164P.

PA (GETH) GENENTECH INC.

PI Simmonds LC, Klimowski L, Reilly DE, Vansura DG;

DR WPI; 2002-619253/66.

DR N-PSDB; ABB86646.

PT New polynucleotide comprising first and second promoter-cistron pairs,
 PT useful for diagnosing, treating or preventing diseases associated with
 PT abnormal expression and/or activity of antigens such as inflammatory
 PT disorders.

PS Disclosure; Fig 21A-C; 104pp; English.

CC The invention provides a polynucleotide, which encodes an immunoglobulin
 CC (Ig), comprising a first or second promoter-cistron pair consisting of a
 CC first or second promoter and cistron, respectively. The first cistron of
 CC the first promoter-cistron pair comprises a first translational
 CC initiation region (TIR-1) operably linked to a nucleic acid sequence
 CC encoding an Ig light chain and the second cistron of the second promoter-
 CC cistron pair comprises a second translational initiation region (TIR-2)
 CC operably linked to a nucleic acid sequence encoding an Ig heavy chain.
 CC Upon expression of the polynucleotide in a prokaryotic host cell, light
 CC and heavy chains are folded and assembled to form a biologically active
 CC Ig. The antibody of the invention is useful for diagnosing, treating or
 CC preventing diseases or conditions associated with abnormal expression and
 CC /or activity of one or more antigen molecules e.g. lymphoid malignancies,
 CC inflammatory, angiogenic, immunologic, neuronal, glial, astrocytic,
 CC hypothalamic or other glandular disorders. The present sequence
 CC represents the amino acid sequence of an anti-vascular endothelial growth
 CC factor (VEGF) light chain fragment of the cistron vector pXVG2AP11
 XX Sequence 237 AA;

Query Match 100.0%; Score 575; DB 5; Length 237;
 Best Local Similarity 100.0%; Pred. No. 1.1e-33;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTSPSSLSASVGRVITTCASODISNYLNMWQKPKAPKVIYFTSSLSHGVPS 60
 DB 24 DIQLTSPSSLSASVGRVITTCASODISNYLNMWQKPKAPKVIYFTSSLSHGVPS 83

QY 61 RFSGSGSGTDFTLTITSLQPEDPATYCCQYSTVPMWTFGGTKVIRKTV 110
 DB 84 RFSGSGSGTDFTLTITSLQPEDPATYCCQYSTVPMWTFGGTKVIRKTV 133

RESULT 8
 ABP51952
 ID ABP51952 standard; protein; 237 AA.
 XX
 AC ABP51952;
 XX
 DT 09-OCT-2002 (first entry)
 XX
 DE Plasmid pY0317 anti-VEGF Fab amino acid sequence SEQ ID NO:2 #1.
 XX
 KM Bacterial host; protease; degP; prc; spr; anti-VEGF antibody; antibody;
 KM humanised; Ap02 ligand; anti-CD18; anti-tissue factor; 2C4; anti-CD20;
 KM anti-vascular endothelial growth factor; anti-Her-2; anti-CD40; Fab;
 KM anti-CD11a; Fab; Fab' 2; Fab' 2-leucine zipper fusion; anti-VEGF Fab.
 XX
 OS Mus sp.
 OS Escherichia coli.
 OS Synthetic.

Key location/Qualifiers
 FT Peptide 1..23
 FT /label= signal
 FT Protein 24..237
 FT /label= anti-VEGF_Fab

MO200248376-A2.
 20-JUN-2002.
 07-DEC-2001; 2001WO-US047581.
 14-DEC-2000; 2000US-0256162P.
 (GETH) GENENTECH INC.
 Chen CY;
 WPI; 2002-583522/62.
 N-PSDB; ABQ73919.

Novel Escherichia coli strain useful for producing polypeptide, deficient in degP and prc encoding protease, and harbouring mutant spr gene, product of gene suppresses growth phenotypes of strains harbouring prc mutants.

Example 1; Fig 1A-C; 63pp; English.

The present invention describes an Escherichia coli strain (I) deficient in chromosomal degP and prc encoding protease and prc, respectively, and harbouring a mutant spr gene, the product of mutant spr gene suppresses growth phenotypes exhibited by strains harbouring prc mutants. (I) is useful for producing a polypeptide, by culturing (I) comprising nucleic acid encoding the polypeptide, which is heterologous to the strain, such that the nucleic acid is expressed, and recovering the heterologous polypeptide from the strain. The heterologous polypeptide is proteolytically sensitive. Culturing of (I) is performed in a fermentor under conditions of high- or low-cell density fermentation. The polypeptide is recovered from the periplasm or culture medium of the strain. The polypeptide is an antibody (humanised or full-length antibody) or Ap02 ligand. The antibody is an anti-CD18, anti-vascular

endothelial growth factor (VEGF), anti-tissue factor, 2C4, anti-Her-2, anti-CD20, anti-CD40, or anti-CD11a antibody. The antibody is also an antibody fragment having a light chain (kappa light chain). The antibody fragment is a Fab, Fab', Fab' 2 or Fab' 2-leucine zipper fusion, anti-CD18 Fab' 2-leucine zipper fusion, anti-tissue factor Fab' 2-leucine zipper fusion or anti-VEGF Fab, with or without a histidine or lysine tag, anti-tissue factor Fab' 2-leucine zipper fusion with a 6-histidine tag, or anti-CD18 Fab' 2-leucine zipper fusion with a 6-histidine tag, and anti-CD18 Fab' 2-leucine zipper fusion with a 6-lysine tag. The present sequence represents an anti-VEGF Fab amino acid sequence from the present invention

Sequence 237 AA:

Query Match 100.0%; Score 575; DB 5; Length 237;
 Best Local Similarity 100.0%; Pred. No. 1.1e-33;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTSPSSLSASVGRVITTCASODISNYLNMWQKPKAPKVIYFTSSLSHGVPS 60
 DB 24 DIQLTSPSSLSASVGRVITTCASODISNYLNMWQKPKAPKVIYFTSSLSHGVPS 83

QY 61 RFSGSGSGTDFTLTITSLQPEDPATYCCQYSTVPMWTFGGTKVIRKTV 110
 DB 84 RFSGSGSGTDFTLTITSLQPEDPATYCCQYSTVPMWTFGGTKVIRKTV 133

RESULT 9
 ID ADO14128
 ID ADO14128 standard; protein; 237 AA.
 XX
 AC ADO14128;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Plasmid pXVG2AP11 expression cassette light chain protein SEQ ID NO:8.
 XX
 KM antibody; variant heavy chain hinge region; immunocombinator; cytostratic;
 KM immunosuppressive; immunotherapy; tumour; cancer; immune disorder;
 KM expression cassette; plasmid pXVG2AP11; anti-VEGF light chain.
 XX
 OS Synthetic.

MO2004042017-A2.
 21-MAY-2004.
 30-OCT-2003; 2003WO-US034610.
 31-OCT-2002; 2002US-0422952P.
 (GETH) GENENTECH INC.
 Reilly D, Yansura DG;
 WPI; 2004-390607/36.
 N-PSDB; ADO14127.

New antibody comprising a variant heavy chain hinge region incapable of inter-heavy chain disulfide linkage, useful for treating, preventing, diagnosing, delaying or preventing a disease, e.g. tumor, cancer or immune disorder.

Example 1; SEQ ID NO 8; 124pp; English.

The present invention describes an antibody comprising a variant heavy chain hinge region incapable of inter-heavy chain disulfide linkage. Also described (1) an antibody lacking inter-heavy chain disulfide linkage; (2) an immunocombinator comprising the antibody conjugated with a heterologous moiety; (3) a composition comprising the antibody or immunocombinator, and carrier; (4) an article of manufacture comprising the composition in a container; (5) a polynucleotide encoding the antibody or immunocombinator, or a variant immunoglobulin heavy chain

CC described: (1) an antibody lacking inter-heavy chain disulfide linkage; (2) an immunconjugate comprising the antibody conjugated with a heterologous moiety; (3) a composition comprising the antibody or

XX Example 2; SEQ ID NO 7; 161pp; English.

XX The present invention describes a method for producing an antibody or
 CC antigen binding fragment in high yield in a cell culture. The method
 CC comprises expressing a variable domain of the antibody or antigen binding
 CC fragment comprising a modified framework region (FR) in a host cell, and
 CC recovering the antibody or antigen binding fragment variable domain
 CC comprising the modified framework from the host cell. The modified FR in
 CC the method described above has a substitution of at least one amino acid
 CC position with a different amino acid, where the different amino acid is
 CC the amino acid found at the corresponding FR position of a human subgroup
 CC variable domain consensus sequence that has a hypervariable region 1
 CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
 CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
 CC The antibody or antigen binding fragment variable domain comprises the
 CC modified FR that has improved yield in cell culture compared to an
 CC unmodified antibody or antigen-binding fragment. The antibody and antigen
 CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and
 CC immunomodulatory activities, and can be used in antibody therapy. The
 CC methods and compositions of the present invention are useful for
 CC producing antibodies or antigen binding fragments in cell culture, in
 CC particular for improving the yield of recombinant antibodies or antigen
 CC binding fragments in cell culture. The antibodies of the invention can be
 CC used to diagnose, treat, inhibit or prevent e.g. tumours and
 CC inflammatory, angiogenic and immunological disorders. The present
 CC sequence represents the light chain of an anti-VEGF (vascular endothelial
 CC cell growth factor) antibody, which is used in the exemplification of the
 CC present invention.

XX Sequence 237 AA;

Query Match 100.0%; Score 575; DB 8; Length 237;
 Best Local Similarity 100.0%; Pred. No. 1,1e-33;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQTGSPSSLSASVGDRTVITCSASQDISNYLNMVQOKPKAKPKVLIYFTSSLSHGVPS 60
 DB 24 DIQTGSPSSLSASVGDRTVITCSASQDISNYLNMVQOKPKAKPKVLIYFTSSLSHGVPS 83

QY 61 RFSGSGSGTDFLTITSSLOPEDPATYVCOQYSTVPMTFGGGTKEIKRTV 110
 DB 84 RFSGSGSGTDFLTITSSLOPEDPATYVCOQYSTVPMTFGGGTKEIKRTV 133

RESULT 12
 ADQ90701
 XX ADQ90701 standard; protein; 237 AA.

AC ADQ90701;

XX 21-OCT-2004 (first entry)

DE Anti-VEGF antibody VNERK light chain protein SEQ ID NO:5.

XX antibody; antigen binding fragment; cell culture; variable domain;
 KW modified framework region; hypervariable region; cytostatic;
 KW antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
 KW tumour; inflammatory disorder; angiogenic disorder;
 KW immunological disorder; anti-VEGF antibody;
 KW anti vascular endothelial cell growth factor antibody; light chain.

OS Homo sapiens.
 OS Synthetic.

PN WO2004065417-A2.

XX 05-AUG-2004.

XX 23-JAN-2004; 2004WO-US001844.

XX 23-JAN-2003; 2003US-0442484P.

XX (GERTH) GENENTECH INC.

XX

PI Simmons L;

XX WPI; 2004-562149/54.
 DR N-PSDB; ADQ90700.

XX Producing an antibody or antigen binding fragment in high yield in a cell
 PT culture, comprising expressing a variable domain with a modified framework
 PT region in a host cell.

XX Example 2; SEQ ID NO 5; 161pp; English.

XX The present invention describes a method for producing an antibody or
 CC antigen binding fragment in high yield in a cell culture. The method
 CC comprises expressing a variable domain of the antibody or antigen binding
 CC fragment comprising a modified framework region (FR) in a host cell, and
 CC recovering the antibody or antigen binding fragment variable domain
 CC comprising the modified framework from the host cell. The modified FR in
 CC the method described above has a substitution of at least one amino acid
 CC position with a different amino acid, where the different amino acid is
 CC the amino acid found at the corresponding FR position of a human subgroup
 CC variable domain consensus sequence that has a hypervariable region 1
 CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
 CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
 CC The antibody or antigen binding fragment variable domain comprises the
 CC modified FR that has improved yield in cell culture compared to an
 CC unmodified antibody or antigen-binding fragment. The antibody and antigen
 CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and
 CC immunomodulatory activities, and can be used in antibody therapy. The
 CC methods and compositions of the present invention are useful for
 CC producing antibodies or antigen binding fragments in cell culture, in
 CC particular for improving the yield of recombinant antibodies or antigen
 CC binding fragments in cell culture. The antibodies of the invention can be
 CC used to diagnose, treat, inhibit or prevent e.g. tumours and
 CC inflammatory, angiogenic and immunological disorders. The present
 CC sequence represents the light chain of an anti-VEGF (vascular endothelial
 CC cell growth factor) antibody, which is used in the exemplification of the
 CC present invention.

XX Sequence 237 AA;

Query Match 100.0%; Score 575; DB 8; Length 237;
 Best Local Similarity 100.0%; Pred. No. 1,1e-33;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQTGSPSSLSASVGDRTVITCSASQDISNYLNMVQOKPKAKPKVLIYFTSSLSHGVPS 60
 DB 24 DIQTGSPSSLSASVGDRTVITCSASQDISNYLNMVQOKPKAKPKVLIYFTSSLSHGVPS 83

QY 61 RFSGSGSGTDFLTITSSLOPEDPATYVCOQYSTVPMTFGGGTKEIKRTV 110
 DB 84 RFSGSGSGTDFLTITSSLOPEDPATYVCOQYSTVPMTFGGGTKEIKRTV 133

RESULT 13
 ADQ90705

XX ADQ90705 standard; protein; 237 AA.

AC ADQ90705;

XX 21-OCT-2004 (first entry)

DE Anti-VEGF antibody VNERK light chain protein SEQ ID NO:9.

XX antibody; antigen binding fragment; cell culture; variable domain;
 KW modified framework region; hypervariable region; cytostatic;
 KW antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
 KW tumour; inflammatory disorder; angiogenic disorder;
 KW immunological disorder; anti-VEGF antibody;
 KW anti vascular endothelial cell growth factor antibody; light chain.

OS Homo sapiens.
 OS Synthetic.

XX

PN WO2004065417-A2.
XX 05-AUG-2004.
XX 23-JAN-2004; 2004WO-US001844.
XX 23-JAN-2003; 2003US-0442484P.
XX (GETH) GENENTECH INC.
XX Stimmone L;
XX WPI; 2004-562149/54.
XX N-PSDB; ADO90704.
XX
XX Producing an antibody or antigen binding fragment in high yield in a cell
XX culture, comprises expressing a variable domain with a modified framework
XX region in a host cell.
XX
XX Example 2; SEQ ID NO 9; 161bp; English.
XX
XX The present invention describes a method for producing an antibody or
XX antigen binding fragment in high yield in a cell culture. The method
XX comprises expressing a variable domain of the antibody or antigen binding
XX fragment comprising a modified framework region (FR) in a host cell, and
XX recovering the antibody or antigen binding fragment variable domain
XX comprising the modified framework from the host cell. The modified FR in
XX the method described above has a substitution of at least one amino acid
XX position with a different amino acid, where the different amino acid is
XX the amino acid found at the corresponding FR position of a human subgroup
XX (HVR1) and/or HVR2 amino acid sequence that has a hypervariable region 1
XX with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
XX The antibody or antigen binding fragment variable domain comprises the
XX modified FR that has improved yield in cell culture compared to an
XX unmodified antibody or antigen-binding fragment. The antibody and antigen
XX binding fragment have cytostatic, antiinflammatory, antiangiogenic and
XX immunomodulatory activities, and can be used in antibody therapy. The
XX methods and compositions of the present invention are useful for
XX producing antibodies or antigen binding fragments in cell culture, in
XX particular for improving the yield of recombinant antibodies or antigen
XX binding fragments in cell culture. The antibodies of the invention can be
XX used to diagnose, treat, inhibit or prevent e.g. tumours and
XX inflammatory, angiogenic and immunological disorders. The present
XX sequence represents the light chain of an anti-VEGF (vascular endothelial
XX cell growth factor) antibody, which is used in the exemplification of the
XX present invention.
XX
XX Sequence 237 AA;
XX
XX
XX Query Match 100.0%; Score 575; DB 8; Length 237;
XX Best Local Similarity 100.0%; Pred. No. 1,1e-33;
XX Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTITCSASODISNYLWYQKPKAKPKVLIYFTSSLHSGVPS 60
DB 24 DIQLTQSPSSLSASVGDRTITCSASODISNYLWYQKPKAKPKVLIYFTSSLHSGVPS 83
QY 61 RFGSGSGGTDFLTITSSLOPEDPATYCCQYSTVPMWTFGGTKVEIKRTV 110
DB 84 RFGSGSGGTDFLTITSSLOPEDPATYCCQYSTVPMWTFGGTKVEIKRTV 133
RESULT 14
ID ADO90709 standard; protein; 237 AA.
XX ADO90709;
XX
XX 21-OCT-2004 (first entry)
XX
XX Anti-VEGF antibody VNERK light chain protein SEQ ID NO:13.
XX

KW antibody; antigen binding fragment; cell culture; variable domain;
KW modified framework region; hypervariable region; cytostatic;
KW antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
KW tumour; inflammatory disorder; angiogenic disorder;
KW immunological disorder; anti-VEGF antibody;
KW anti vascular endothelial cell growth factor antibody; light chain.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO2004065417-A2.
XX 05-AUG-2004.
XX 23-JAN-2004; 2004WO-US001844.
XX 23-JAN-2003; 2003US-0442484P.
XX (GETH) GENENTECH INC.
XX Stimmone L;
XX WPI; 2004-562149/54.
XX N-PSDB; ADO90708.
XX
XX Producing an antibody or antigen binding fragment in high yield in a cell
XX culture, comprises expressing a variable domain with a modified framework
XX region in a host cell.
XX
XX Example 2; SEQ ID NO 13; 161bp; English.
XX
XX The present invention describes a method for producing an antibody or
XX antigen binding fragment in high yield in a cell culture. The method
XX comprises expressing a variable domain of the antibody or antigen binding
XX fragment comprising a modified framework region (FR) in a host cell, and
XX recovering the antibody or antigen binding fragment variable domain
XX comprising the modified framework from the host cell. The modified FR in
XX the method described above has a substitution of at least one amino acid
XX position with a different amino acid, where the different amino acid is
XX the amino acid found at the corresponding FR position of a human subgroup
XX (HVR1) and/or HVR2 amino acid sequence that has a hypervariable region 1
XX with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
XX The antibody or antigen binding fragment variable domain comprises the
XX modified FR that has improved yield in cell culture compared to an
XX unmodified antibody or antigen-binding fragment. The antibody and antigen
XX binding fragment have cytostatic, antiinflammatory, antiangiogenic and
XX immunomodulatory activities, and can be used in antibody therapy. The
XX methods and compositions of the present invention are useful for
XX producing antibodies or antigen binding fragments in cell culture, in
XX particular for improving the yield of recombinant antibodies or antigen
XX binding fragments in cell culture. The antibodies of the invention can be
XX used to diagnose, treat, inhibit or prevent e.g. tumours and
XX inflammatory, angiogenic and immunological disorders. The present
XX sequence represents the light chain of an anti-VEGF (vascular endothelial
XX cell growth factor) antibody, which is used in the exemplification of the
XX present invention.
XX
XX Sequence 237 AA;
XX
XX
XX Query Match 100.0%; Score 575; DB 8; Length 237;
XX Best Local Similarity 100.0%; Pred. No. 1,1e-33;
XX Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTITCSASODISNYLWYQKPKAKPKVLIYFTSSLHSGVPS 60
DB 24 DIQLTQSPSSLSASVGDRTITCSASODISNYLWYQKPKAKPKVLIYFTSSLHSGVPS 83
QY 61 RFGSGSGGTDFLTITSSLOPEDPATYCCQYSTVPMWTFGGTKVEIKRTV 110
DB 84 RFGSGSGGTDFLTITSSLOPEDPATYCCQYSTVPMWTFGGTKVEIKRTV 133

RESULT 15

ADQ90723

ID ADQ90723 standard; protein; 237 AA.

AC ADQ90723;

DT 21-OCT-2004 (first entry)

DE Anti-VEGF antibody VNERK light chain protein SEQ ID NO:27.

KW antibody; antigen binding fragment; cell culture; variable domain;

KW modified framework region; hypervariable region; cytosolic;

KW tumour; inflammatory disorder; angiogenic disorder;

KW immunological disorder; anti-VEGF antibody;

KW anti vascular endothelial cell growth factor antibody; light chain.

OS Homo sapiens.

PN WO2004065417-A2.

PD 05-AUG-2004.

PF 23-JAN-2004; 2004WO-US001844.

PR 23-JAN-2003; 2003US-0442484P.

PA (GETH) GENENTECH INC.

PI Simmons L;

DR WPI; 2004-562149/54.

DR N-PSDB; ADQ90722.

PT Producing an antibody or antigen binding fragment in high yield in a cell

PT culture, comprises expressing a variable domain with a modified framework

PT region in a host cell.

PS Example 7; SEQ ID NO 27; 161pp; English.

XX The present invention describes a method for producing an antibody or
 CC antigen binding fragment in high yield in a cell culture. The method
 CC comprises expressing a variable domain of the antibody or antigen binding
 CC fragment comprising a modified framework region (FR) in a host cell, and
 CC recovering the antibody or antigen binding fragment variable domain
 CC comprising the modified framework from the host cell. The modified FR in
 CC the method described above has a substitution of at least one amino acid
 CC position with a different amino acid, where the different amino acid is
 CC the amino acid found at the corresponding FR position of a human subgroup
 CC (HVR1) and/or HVR2 amino acid sequence that has a hypervariable region 1
 CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
 CC The antibody or antigen binding fragment variable domain comprises the
 CC modified FR that has improved yield in cell culture compared to an
 CC unmodified antibody or antigen-binding fragment. The antibody and antigen
 CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and
 CC immunomodulatory activities, and can be used in antibody therapy. The
 CC methods and compositions of the present invention are useful for
 CC producing antibodies or antigen binding fragments in cell culture, in
 CC particular for improving the yield of recombinant antibodies or antigen
 CC binding fragments in cell culture. The antibodies of the invention can be
 CC used to diagnose, treat, inhibit or prevent e.g. tumours and
 CC inflammatory, angiogenic and immunological disorders. The present
 CC sequence represents the light chain of an anti-VEGF (vascular endothelial
 CC cell growth factor) antibody, which is used in the exemplification of the
 CC present invention.

SQ Sequence 237 AA;

Query Match

100.0%; Score 575; DB 8; Length 237;

Best Local Similarity 100.0%; Pred. No. 1,1e-33; Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVCDPRVTITCSASODISNYLNMVQOKRGAAPKYLIVETSSLSHGVPS 60
 DB 24 DIQLTQSPSSLSASVCDPRVTITCSASODISNYLNMVQOKRGAAPKYLIVETSSLSHGVPS 83
 QY 61 RPSGSGSGTDFLTITSSLOPEDPATYCCQYSTVPTWTFGQGTKEIKRTV 110
 DB 84 RPSGSGSGTDFLTITSSLOPEDPATYCCQYSTVPTWTFGQGTKEIKRTV 133

Search completed: March 14, 2005, 20:39:16
 Job time : 88.0482 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2005, 20:30:13 ; Search time 22.6754 Seconds
(without alignments)
362.127 Million cell updates/sec

Title: US-09-723-752B-115
Perfect score: 575
Sequence: 1 DIQLTGSPSSLSASVGRVT.....YSTVPMFGQTKYIKRTV 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfiles.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	573	99.7	110	4	US-09-440-781-94
2	569	99.0	491	4	US-10-011-125A-2
3	556	96.7	110	4	US-09-440-781-95
4	522	90.8	214	2	US-07-934-373C-40
5	522	90.8	214	2	US-08-788-800-11
6	522	90.8	214	3	US-08-437-642B-40
7	522	90.8	214	3	US-09-097-1309-2
8	522	90.8	214	3	US-09-097-1309-2
9	522	90.8	214	3	US-09-460-587-2
10	522	90.8	214	4	US-09-940-166A-2
11	522	90.8	214	5	PCT-US93-07832-40
12	522	90.8	233	2	US-07-934-373C-25
13	522	90.8	233	3	US-08-437-642B-25
14	522	90.8	233	4	US-08-146-206C-25
15	522	90.8	233	4	US-09-705-686-25
16	522	90.8	233	4	US-09-705-392A-25
17	522	90.8	233	4	US-09-705-398-25
18	522	90.8	233	5	PCT-US93-07832-25
19	522	90.8	237	3	US-09-097-1309-6
20	522	90.8	237	3	US-09-097-1309-6
21	522	90.8	237	3	US-09-423-712B-2
22	522	90.8	237	3	US-09-607-756-2
23	522	90.8	237	3	US-09-460-587-6
24	522	90.8	237	4	US-09-940-166A-6
25	519	90.3	214	1	US-08-458-516-12
26	518	90.1	109	2	US-07-934-373C-47
27	518	90.1	109	3	US-08-437-642B-47

28	514	89.4	214	2	US-07-934-373C-39	Sequence 39, Appl
29	514	89.4	214	3	US-08-437-642B-39	Sequence 39, Appl
30	514	89.4	214	5	PCT-US93-07832-39	Sequence 39, Appl
31	511	88.9	107	2	US-07-934-373C-17	Sequence 17, Appl
32	511	88.9	107	3	US-08-437-642B-17	Sequence 17, Appl
33	511	88.9	107	4	US-08-146-206C-17	Sequence 17, Appl
34	511	88.9	107	4	US-09-705-686-17	Sequence 17, Appl
35	511	88.9	107	4	US-09-705-392A-17	Sequence 17, Appl
36	511	88.9	107	4	US-09-705-398-17	Sequence 17, Appl
37	511	88.9	107	5	PCT-US93-07832-17	Sequence 17, Appl
38	511	88.9	108	3	US-08-974-899-3	Sequence 3, Appl1
39	511	88.9	108	4	US-09-795-798-3	Sequence 3, Appl1
40	511	88.9	127	3	US-08-649-100-33	Sequence 33, Appl
41	507	88.2	109	2	US-07-934-373C-3	Sequence 3, Appl1
42	507	88.2	109	3	US-08-437-642B-3	Sequence 3, Appl1
43	507	88.2	109	4	US-08-146-206C-3	Sequence 3, Appl1
44	507	88.2	109	4	US-09-705-686-3	Sequence 3, Appl1
45	507	88.2	109	4	US-09-705-392A-3	Sequence 3, Appl1

ALIGNMENTS

```
RESULT 1
US-09-440-781-94
Sequence 94, Application US/09440781
Patent No. 6632826
GENERAL INFORMATION:
APPLICANT: Yvonne Man-yea Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 94
LENGTH: 110
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-110
OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-94

Query Match 99.7%; Score 573; DB 4; Length 110;
Best Local Similarity 99.1%; Pred. No. 8.6e-47;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 DIQLTGSPSSLSASVGRVTITCSASODISYLNWYQKPKAKRVLITFTSLHSGVPS 60
Db 1 DIQLTGSPSSLSASVGRVITCSASODISYLNWYQKPKAKRVLITFTSLHSGVPS 60
Cy 61 RFSSSGGTFTLTITSSLOPEDFATYVCOQSTVPMFGQTKYIKRTV 110
Db 61 RFSSSGGTFTLTITSSLOPEDFATYVCOQSTVPMFGQTKYIKRTV 110

RESULT 2
US-10-011-125A-2
Sequence 2, Application US/10011125A
Patent No. 6828121
GENERAL INFORMATION:
APPLICANT: Chen, Christina Yu-Ching
TITLE OF INVENTION: BACTERIAL HOST STRAINS
FILE REFERENCE: P1804R1
CURRENT APPLICATION NUMBER: US/10/011,125A
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 2
LENGTH: 491
TYPE: PRT
```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6828121
US-10-011-125A-2

Query Match          99.0%; Score 569; DB 4; Length 491;
Best Local Similarity 98.2%; Pred. No. 1.1e-45;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQKPKAPKVLITYFTSSLHSGVPS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 24 DIQLTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQKPKAPKVLITYFTSSLHSGVPS 83
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 RFSGSGSGTDFTLTITSLQPEDPATYCCQYSTVPMTFGQGTVEIKRTV 110
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 84 RFSGSGSGTDYTLTITSLQPEDPATYCCQYSTVPMTFGQGTVEIKRTV 133
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
US-09-440-781-95
; Sequence 95, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-yea Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 95
; LENGTH: 110
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-110
; OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-95

Query Match          96.7%; Score 556; DB 4; Length 110;
Best Local Similarity 95.5%; Pred. No. 3.4e-45;
Matches 105; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQKPKAPKVLITYFTSSLHSGVPS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQLTQSPSSLSASVGDRTVITCRANEQSLNYLNMWYQKPKAPKVLITYFTSSLHSGVPS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 RFSGSGSGTDFTLTITSLQPEDPATYCCQYSTVPMTFGQGTVEIKRTV 110
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFSGSGSGTDFTLTITSLQPEDPATYCCQYSTVPMTFGQGTVEIKRTV 110
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
US-07-934-373C-40
; Sequence 40, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```

; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-40

Query Match          90.8%; Score 522; DB 2; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1e-41;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQKPKAPKVLITYFTSSLHSGVPS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQDISNYLNMWYQKPKAPKVLITYFTSSLHSGVPS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 RFSGSGSGTDFTLTITSLQPEDPATYCCQYSTVPMTFGQGTVEIKRTV 110
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFSGSGSGTDYTLTITSLQPEDPATYCCQYSTVPMTFGQGTVEIKRTV 110
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
US-08-788-800-11
; Sequence 11, Application US/08788800
; Patent No. 5914112
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
; FILING DATE: 22-Jan-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0887x1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 11:
```


SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-788-800-11

Query Match 90.8%; Score 522; DB 3; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1e-41;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITTCASQDISNYLNMWYQKPKAKPVLIYFTSLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITTCRASQDINNINLMWYQKPKAKPKLIIYFTSLHSGVPS 60
QY 61 RFSGSGSGTDFTLTISLSLOPEDFATYYCQOYSTVPMFGGTKEIKRTV 110
DB 61 RFSGSGSGTDYTLTISLSLOPEDFATYYCQOQNTLPTFGGTKEIKRTV 110

RESULT 6

US-08-437-642B-40
Sequence 40, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
City: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437, 642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-40

Query Match 90.8%; Score 522; DB 3; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1e-41;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITTCASQDISNYLNMWYQKPKAKPVLIYFTSLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITTCRASQDINNINLMWYQKPKAKPKLIIYFTSLHSGVPS 60
QY 61 RFSGSGSGTDFTLTISLSLOPEDFATYYCQOYSTVPMFGGTKEIKRTV 110
DB 61 RFSGSGSGTDYTLTISLSLOPEDFATYYCQOQNTLPTFGGTKEIKRTV 110

RESULT 7

US-09-097-309-2
Sequence 2, Application US/09097309
Patent No. 6121428
GENERAL INFORMATION:
APPLICANT: Blank, Gregory S.
APPLICANT: Natindray, Daljit S.
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: Protein Recovery
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
City: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097, 309
FILING DATE: 12-Jun-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050951
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-7467
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-097-309-2

Query Match 90.8%; Score 522; DB 3; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1e-41;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITTCASQDISNYLNMWYQKPKAKPVLIYFTSLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITTCRASQDINNINLMWYQKPKAKPKLIIYFTSLHSGVPS 60
QY 61 RFSGSGSGTDFTLTISLSLOPEDFATYYCQOYSTVPMFGGTKEIKRTV 110
DB 61 RFSGSGSGTDYTLTISLSLOPEDFATYYCQOQNTLPTFGGTKEIKRTV 110

RESULT 8

US-09-097-171A-2
Sequence 2, Application US/09097171A
Patent No. 6171586
GENERAL INFORMATION:
APPLICANT: Lam, Xanthie M.
APPLICANT: Oeswein, James Q.

APPLICANT: Ongpattanakul, Boonart
APPLICANT: Shantokh, Zaira
APPLICANT: Wang, Sharon X.
APPLICANT: Weisburg, Robert P.
APPLICANT: Wong, Rita L.
TITLE OF INVENTION: Antibody Formulation
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,171A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/874897
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1089R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
FAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-097-171A-2
Query Match
Best Local Similarity 90.8%; Score 522; DB 3; Length 214;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTVITTCASQDISNINMYQKPGKAPKLLIYFTSLHSGVPS 60
DB 1 DIQLTQSPSSLSASVGDRTVITTCASQDISNINMYQKPGKAPKLLIYFTSLHSGVPS 60
QY 61 RFGSGSGTDFTLTLSISLPEDPAATYYCOQSTVPTFGQTKVEIKRTV 110
DB 61 RFGSGSGTDFTLTLSISLPEDPAATYYCOQSTVPTFGQTKVEIKRTV 110
RESULT 9
US-09-460-587-2
Sequence 2, Application US/09460587
Patent No. 6322997
GENERAL INFORMATION:
APPLICANT: Blank, Gregory S.
APPLICANT: Narindray, Daljit S.
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: Protein Recovery
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/460,587
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/097,309
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-7467
FAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-460-587-2
Query Match
Best Local Similarity 90.8%; Score 522; DB 3; Length 214;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTVITTCASQDISNINMYQKPGKAPKLLIYFTSLHSGVPS 60
DB 1 DIQLTQSPSSLSASVGDRTVITTCASQDISNINMYQKPGKAPKLLIYFTSLHSGVPS 60
QY 61 RFGSGSGTDFTLTLSISLPEDPAATYYCOQSTVPTFGQTKVEIKRTV 110
DB 61 RFGSGSGTDFTLTLSISLPEDPAATYYCOQSTVPTFGQTKVEIKRTV 110
RESULT 10
US-09-940-166A-2
Sequence 2, Application US/09940166A
Patent No. 6716598
GENERAL INFORMATION:
APPLICANT: Blank, Gregory S.
APPLICANT: Narindray, Daljit S.
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: Protein Recovery
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/940,166A
FILING DATE: 27-Aug-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/097,309
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-7467
FAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-940-166A-2

Query Match 90.8%; Score 522, DB 4; Length 214;
Best Local Similarity 90.0%; Pred. No. 1,1e-41;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQLTGSPSSLSASVGRVTITCGASQDINNLYMWYQKPKAPKLLIYTTSLHSGVPS 60
DB 1 DIQLTGSPSSLSASVGRVTITCGASQDINNLYMWYQKPKAPKLLIYTTSLHSGVPS 60
QY 61 RFSGSGGTDTLTITSLQPEDPATYCCQGYSTVPMTFGGTKVEIKRTV 110
DB 61 RFSGSGGTDTLTITSLQPEDPATYCCQGYSTVPMTFGGTKVEIKRTV 110

RESULT 11
PCT-US93-07832-40

Sequence 40, Application PC/TUS9307832
GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants

NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd

CITY: South San Francisco
STATE: California

COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820

CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/115272
FILING DATE: 14-JUN-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126

FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992

ATTORNEY/AGENT INFORMATION:
NAME:

REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 709P2PCT

TELECOMMUNICATION INFORMATION:
TELEPHONE:

TELEFAX: 415/952-9881
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:

LENGTH: 214 amino acids
TYPE: amino acid

TOPOLOGY: Linear
PCT-US93-07832-40

Query Match 90.8%; Score 522, DB 5; Length 214;
Best Local Similarity 90.0%; Pred. No. 1,1e-41;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQLTGSPSSLSASVGRVTITCGASQDINNLYMWYQKPKAPKLLIYTTSLHSGVPS 60
DB 1 DIQLTGSPSSLSASVGRVTITCGASQDINNLYMWYQKPKAPKLLIYTTSLHSGVPS 60

DB 1 DIQLTGSPSSLSASVGRVTITCGASQDINNLYMWYQKPKAPKLLIYTTSLHSGVPS 60
QY 61 RFSGSGGTDTLTITSLQPEDPATYCCQGYSTVPMTFGGTKVEIKRTV 110
DB 61 RFSGSGGTDTLTITSLQPEDPATYCCQGYSTVPMTFGGTKVEIKRTV 110

RESULT 12
US-07-934-373C-25

Sequence 25, Application US/07934373C
Patent No. 5821337

GENERAL INFORMATION:
APPLICANT: Paul J. Carter

TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way
CITY: South San Francisco

STATE: California
COUNTRY: USA

ZIP: 94080
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C

FILING DATE: 21-Aug-1992
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126

FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991

ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994

TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids

TYPE: Amino Acid
TOPOLOGY: Linear

US-07-934-373C-25

Query Match 90.8%; Score 522, DB 2; Length 233;
Best Local Similarity 90.0%; Pred. No. 1,3e-41;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQLTGSPSSLSASVGRVTITCGASQDINNLYMWYQKPKAPKLLIYTTSLHSGVPS 60
DB 20 DIQLTGSPSSLSASVGRVTITCGASQDINNLYMWYQKPKAPKLLIYTTSLHSGVPS 79
QY 61 RFSGSGGTDTLTITSLQPEDPATYCCQGYSTVPMTFGGTKVEIKRTV 110
DB 80 RFSGSGGTDTLTITSLQPEDPATYCCQGYSTVPMTFGGTKVEIKRTV 129

RESULT 13
US-08-437-642B-25

Sequence 25, Application US/08437642B
Patent No. 6054297

GENERAL INFORMATION:
APPLICANT: Paul J. Carter

ADDRESSEE: Leonard G. Prestea
TITLE OF INVENTION: Immunoglobulin Variants

NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-25

Query Match 90.8%; Score 522; DB 3; Length 233;
Best Local Similarity 90.0%; Pred. No. 1.3e-41;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGVDRVTITCSASODISNTLNMWYQOKPKAPKVLITYFTSLHSGVPS 60
DB 20 DIQMTQSPSSLSASVGVDRVTITCRASODINNTLNMWYQOKPKAPKVLITYFTSLHSGVPS 79

QY 61 RFSGSGSGTDFTLTITSLQPEDPATYCCQYSTVPWTFGQGTKEIKRTV 110
DB 80 RFSGSGSGTDYTLTITSLQPEDPATYCCQGNLTLPFTFGQGTKEIKRTV 129

RESULT 14
US-08-146-206C-25
Sequence 25, Application US/08146206C
Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Prestea, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-No. 6407213-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-146-206C-25

Query Match 90.8%; Score 522; DB 4; Length 233;
Best Local Similarity 90.0%; Pred. No. 1.3e-41;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGVDRVTITCSASODISNTLNMWYQOKPKAPKVLITYFTSLHSGVPS 60
DB 20 DIQMTQSPSSLSASVGVDRVTITCRASODINNTLNMWYQOKPKAPKVLITYFTSLHSGVPS 79

QY 61 RFSGSGSGTDFTLTITSLQPEDPATYCCQYSTVPWTFGQGTKEIKRTV 110
DB 80 RFSGSGSGTDYTLTITSLQPEDPATYCCQGNLTLPFTFGQGTKEIKRTV 129

RESULT 15
US-09-705-686-25
Sequence 25, Application US/09705686
Patent No. 6639055
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Prestea, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-No. 6639055-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D3
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-705-686-25

Query Match 90.8%; Score 522; DB 4; Length 233;
Best Local Similarity 90.0%; Pred. No. 1.3e-41;
Matches 99; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY	1	DIQLTQSPSSISASVGDRTITCSASODISNYLNMWYQKPGKAPKVLITYFTSLHSGVPS	60
DB	20	DIQWTQSPSSISASVGDRTITCRASQDINNYLNMWYQKPGKAPKVLITYFTSLHSGVPS	79
QY	61	RFGSGSGCTDFTLTISSIQPEDFATYYCOQYSTVPMTFGQGTKEIKRTV	110
DB	80	RFGSGSGCTDFTLTISSIQPEDFATYYCOQGNLTPTFGQGTKEIKRTV	129

Search completed: March 14, 2005, 20:43:52
Job time : 22.6754 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2005, 20:22:02 ; Search time 41.0088 Seconds

(without alignments)
884.760 Million cell updates/sec

Title: US-09-723-752B-115

Perfect score: 575
Sequence: 1 DIQLTQSPSLASVGDRTV.....YSTVPTFGQGTVEIKRTV 110Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubppaa/PCF_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubppaa/PCFUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubppaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubppaa/US09C_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubppaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubppaa/US10D_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	575	100.0	110	9	US-09-056-160B-107
2	575	100.0	110	9	US-09-056-160B-117
3	575	100.0	110	14	US-10-234-671-105
4	575	100.0	110	14	US-10-234-671-115
5	575	100.0	213	16	US-10-379-392-135
6	575	100.0	213	16	US-10-379-392-137
7	575	100.0	213	16	US-10-379-392-139
8	575	100.0	214	15	US-10-364-953-1
9	575	100.0	237	14	US-10-020-786-10
10	575	100.0	237	17	US-10-697-995-8
11	575	100.0	237	17	US-10-697-995-11
12	573	99.7	110	14	US-10-234-671-8
13	573	99.7	110	15	US-10-624-153-94

14	572	99.5	110	9	US-09-056-160B-105	Sequence 105, App
15	572	99.5	110	14	US-10-234-671-103	Sequence 103, App
16	571	99.3	213	16	US-10-379-392-155	Sequence 155, App
17	570	99.1	213	16	US-10-379-392-153	Sequence 153, App
18	569	99.0	110	9	US-09-056-160B-103	Sequence 103, App
19	569	99.0	110	14	US-10-234-671-101	Sequence 101, App
20	569	99.0	237	9	US-09-056-160B-100	Sequence 100, App
21	569	99.0	237	14	US-10-234-671-100	Sequence 100, App
22	569	99.0	491	13	US-10-379-392-125-2	Sequence 2, App
23	567	98.6	213	13	US-10-379-392-157	Sequence 157, App
24	566	98.4	108	13	US-10-153-159-4	Sequence 4, App11
25	566	98.4	108	15	US-10-153-176-4	Sequence 4, App11
26	566	98.4	108	15	US-10-443-134A-4	Sequence 4, App11
27	564	98.1	108	9	US-09-056-160B-8	Sequence 8, App11
28	564	98.1	108	13	US-10-153-159-2	Sequence 2, App11
29	564	98.1	108	13	US-10-153-159-16	Sequence 16, App1
30	564	98.1	108	14	US-10-153-176-2	Sequence 2, App11
31	564	98.1	108	14	US-10-153-176-16	Sequence 16, App1
32	564	98.1	108	15	US-10-443-134A-2	Sequence 2, App11
33	564	98.1	108	15	US-10-443-134A-16	Sequence 16, App1
34	564	98.1	108	15	US-10-443-134A-127	Sequence 127, App
35	564	98.1	108	17	US-10-877-532-7	Sequence 7, App11
36	561	97.6	108	9	US-09-056-160B-126	Sequence 126, App
37	561	97.6	108	14	US-10-234-671-124	Sequence 124, App
38	559	97.2	107	16	US-10-723-434-1	Sequence 1, App11
39	558	97.0	214	15	US-10-364-953-4	Sequence 4, App11
40	557	96.9	214	15	US-10-364-953-3	Sequence 3, App11
41	556	96.7	107	9	US-09-056-160B-13	Sequence 13, App1
42	556	96.7	107	14	US-10-234-671-13	Sequence 13, App1
43	556	96.7	110	9	US-09-056-160B-109	Sequence 109, App
44	556	96.7	110	9	US-09-056-160B-111	Sequence 111, App
45	556	96.7	110	9	US-09-056-160B-113	Sequence 113, App

ALIGNMENTS

RESULT 1
US-09-056-160B-107
Sequence 107, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Beca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haeak, Janet B.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-107

Query Match 100.0%; Score 575; DB 9; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.8e-40;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCSASODISNYLWYQKRGKAPKVLITYFTSSLSHSGVPS 60
DB 1 DIQLTQSPSSLSASVGDRTVITCSASODISNYLWYQKRGKAPKVLITYFTSSLSHSGVPS 60
QY 61 RFGSGSGTDFTLTISLQPEDPATYCCOYSTVPMTFGGTVEIKRTV 110
DB 61 RFGSGSGTDFTLTISLQPEDPATYCCOYSTVPMTFGGTVEIKRTV 110

RESULT 2

US-09-056-160B-117
Sequence 117, Application US/09056160B
Patent No. US20020032315A1

GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haseak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-117

Query Match 100.0%; Score 575; DB 9; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.8e-40;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCSASODISNYLWYQKRGKAPKVLITYFTSSLSHSGVPS 60
DB 1 DIQLTQSPSSLSASVGDRTVITCSASODISNYLWYQKRGKAPKVLITYFTSSLSHSGVPS 60

DB 1 DIQLTQSPSSLSASVGDRTVITCSASODISNYLWYQKRGKAPKVLITYFTSSLSHSGVPS 60

QY 61 RFGSGSGTDFTLTISLQPEDPATYCCOYSTVPMTFGGTVEIKRTV 110
DB 61 RFGSGSGTDFTLTISLQPEDPATYCCOYSTVPMTFGGTVEIKRTV 110

RESULT 3

US-10-234-671-105
Sequence 105, Application US/10234671
Publication No. US20030190317A1

GENERAL INFORMATION:
APPLICANT: Baca, Manuel

Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.

TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671

FILING DATE: 03-Sep-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160

FILING DATE: 06-Apr-1998

APPLICATION NUMBER: 60/126446

FILING DATE: 07-Apr-1997

APPLICATION NUMBER: 60/054856

FILING DATE: 06-AUG-1997

ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.

REGISTRATION NUMBER: 44,637

REFERENCE/DOCKET NUMBER: P1093R2C1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:

LENGTH: 110 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-234-671-105

Query Match 100.0%; Score 575; DB 14; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.8e-40;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCSASODISNYLWYQKRGKAPKVLITYFTSSLSHSGVPS 60
DB 1 DIQLTQSPSSLSASVGDRTVITCSASODISNYLWYQKRGKAPKVLITYFTSSLSHSGVPS 60
QY 61 RFGSGSGTDFTLTISLQPEDPATYCCOYSTVPMTFGGTVEIKRTV 110
DB 61 RFGSGSGTDFTLTISLQPEDPATYCCOYSTVPMTFGGTVEIKRTV 110

RESULT 4

US-10-234-671-115
Sequence 115, Application US/10234671

Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Welle, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-SEP-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-10-234-671-115
Query Match 100.0%; Score 575; DB 14; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.8e-40;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIQLTQSPSSLSASVGVDRVTITCSASODISNYLNMWYQKPKGKAPKVLITYFTSSLHSGVPS 60
Db 1 DIQLTQSPSSLSASVGVDRVTITCSASODISNYLNMWYQKPKGKAPKVLITYFTSSLHSGVPS 60
Qy 61 RPSGSGGTDFLTITSSIQPEDPATYCCQYSTVPMWFGGQTKVEIKRTV 110
Db 61 RPSGSGGTDFLTITSSIQPEDPATYCCQYSTVPMWFGGQTKVEIKRTV 110
RESULT 5
US-10-379-392-135
Sequence 135, Application US/10379392
Publication No. US20040110226A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
Deesjarlais, John Rudolf
APPLICANT: Marshall, Shannon Alicia
APPLICANT: Dahlvat, Baesil I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR FILING DATE: 2002-05-29
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
SEQ ID NO 135
LENGTH: 213
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Humanized
US-10-379-392-135
Query Match 100.0%; Score 575; DB 16; Length 213;
Best Local Similarity 100.0%; Pred. No. 3.3e-40;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIQLTQSPSSLSASVGVDRVTITCSASODISNYLNMWYQKPKGKAPKVLITYFTSSLHSGVPS 60
Db 1 DIQLTQSPSSLSASVGVDRVTITCSASODISNYLNMWYQKPKGKAPKVLITYFTSSLHSGVPS 60
Qy 61 RPSGSGGTDFLTITSSIQPEDPATYCCQYSTVPMWFGGQTKVEIKRTV 110
Db 61 RPSGSGGTDFLTITSSIQPEDPATYCCQYSTVPMWFGGQTKVEIKRTV 110
RESULT 6
US-10-379-392-137
Sequence 137, Application US/10379392
Publication No. US20040110226A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
Deesjarlais, John Rudolf
APPLICANT: Marshall, Shannon Alicia
APPLICANT: Dahlvat, Baesil I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR FILING DATE: 2002-05-29
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
SEQ ID NO 137
LENGTH: 213
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-379-392-137
Query Match 100.0%; Score 575; DB 16; Length 213;
Best Local Similarity 100.0%; Pred. No. 3.3e-40;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIQLTQSPSSLSASVGVDRVTITCSASODISNYLNMWYQKPKGKAPKVLITYFTSSLHSGVPS 60
Db 1 DIQLTQSPSSLSASVGVDRVTITCSASODISNYLNMWYQKPKGKAPKVLITYFTSSLHSGVPS 60
Qy 61 RPSGSGGTDFLTITSSIQPEDPATYCCQYSTVPMWFGGQTKVEIKRTV 110
Db 61 RPSGSGGTDFLTITSSIQPEDPATYCCQYSTVPMWFGGQTKVEIKRTV 110
RESULT 7
US-10-379-392-139
Sequence 139, Application US/10379392
Publication No. US20040110226A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan

```

; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Basel I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 139
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (116)..(116)
; OTHER INFORMATION: Xaa at position 116 can be Phe or Tyr
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (133)..(133)
; OTHER INFORMATION: Xaa at position 133 can be Ile, Met or Val
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (135)..(135)
; OTHER INFORMATION: Xaa at position 135 can be Leu, Ile or Met
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (176)..(176)
; OTHER INFORMATION: Xaa at position 176 can be Met, Val, Ala or Ser
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (178)..(178)
; OTHER INFORMATION: Xaa at position 178 can be Met, Thr or Val
; US-10-379-392-139

Query Match          100.0%; Score 575; DB 16; Length 213;
Best Local Similarity 100.0%; Pred. No. 3.3e-40;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTITCSASQDISNTLNMWQKRGKAPKVLITYFTSSLHSGVPS 60
   |||||
Db 1 DIQLTQSPSSLSASVGDRTITCSASQDISNTLNMWQKRGKAPKVLITYFTSSLHSGVPS 60

QY 61 RFGSGSGTDFTLTISLQPEDPATYCCQYSTVPMWTFGGGTVEIKRTV 110
   |||||
Db 61 RFGSGSGTDFTLTISLQPEDPATYCCQYSTVPMWTFGGGTVEIKRTV 110

RESULT 8
; US-10-364-953-1
; Sequence 1, Application US/10364953
; Publication No. US20030224397A1
; GENERAL INFORMATION:
; APPLICANT: LOWMAN, HENRY B.
; APPLICANT: KARVIN, JONATHAN S.
; TITLE OF INVENTION: ANTIBODY VARIANTS WITH FASTER ANTIGEN ASSOCIATION RATES
; FILE REFERENCE: P1951R1
; CURRENT APPLICATION NUMBER: US/10/364,953
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/355,895
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/409,685
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 1
; LENGTH: 214
; TYPE: PRT
```

```

; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: Artificial sequence
; LOCATION: Full
; OTHER INFORMATION: Y0101-VL
; US-10-364-953-1

Query Match          100.0%; Score 575; DB 15; Length 214;
Best Local Similarity 100.0%; Pred. No. 3.4e-40;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTITCSASQDISNTLNMWQKRGKAPKVLITYFTSSLHSGVPS 60
   |||||
Db 1 DIQLTQSPSSLSASVGDRTITCSASQDISNTLNMWQKRGKAPKVLITYFTSSLHSGVPS 60

QY 61 RFGSGSGTDFTLTISLQPEDPATYCCQYSTVPMWTFGGGTVEIKRTV 110
   |||||
Db 61 RFGSGSGTDFTLTISLQPEDPATYCCQYSTVPMWTFGGGTVEIKRTV 110

RESULT 9
; US-10-020-786-10
; Sequence 10, Application US/10020786
; Publication No. US20030073164A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Laura C.
; APPLICANT: Klimowski, Laura
; APPLICANT: Reilly, Dorothea
; APPLICANT: Yansura, Daniel G.
; TITLE OF INVENTION: PROKARYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF
; FILE REFERENCE: P1793R1
; CURRENT APPLICATION NUMBER: US/10/020,786
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/256,164
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 10
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: anti-VBGF light chain
; US-10-020-786-10

Query Match          100.0%; Score 575; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 3.7e-40;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTITCSASQDISNTLNMWQKRGKAPKVLITYFTSSLHSGVPS 60
   |||||
Db 24 DIQLTQSPSSLSASVGDRTITCSASQDISNTLNMWQKRGKAPKVLITYFTSSLHSGVPS 83

QY 61 RFGSGSGTDFTLTISLQPEDPATYCCQYSTVPMWTFGGGTVEIKRTV 110
   |||||
Db 84 RFGSGSGTDFTLTISLQPEDPATYCCQYSTVPMWTFGGGTVEIKRTV 133

RESULT 10
; US-10-697-995-8
; Sequence 8, Application US/10697995
; Publication No. US20050048572A1
; GENERAL INFORMATION:
; APPLICANT: Reilly, Dorothea
; APPLICANT: Yansura, Daniel G.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INCREASING ANTIBODY PRODUCTION
; FILE REFERENCE: 11669.195USU1
; CURRENT APPLICATION NUMBER: US/10/697,995
; CURRENT FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: US 60/422,952
; PRIOR FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 37
; SEQ ID NO 8
; LENGTH: 237
```

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: anti-VEGF light chain
US-10-697-995-8

Query Match 100.0%; Score 575; DB 17; Length 237;
Best Local Similarity 100.0%; Pred. No. 3.7e-40;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTSPSSLSASVGDRTVITCSASODISNLYNMYQOKPGKAPKVLIFTSSLSHGVPS 60
DB 24 DIQLTSPSSLSASVGDRTVITCSASODISNLYNMYQOKPGKAPKVLIFTSSLSHGVPS 83
QY 61 RFGSGSGTDFLTITSLQPEDPATYCCQYSTVPMTFGGTVEIKRTV 110
DB 84 RFGSGSGTDFLTITSLQPEDPATYCCQYSTVPMTFGGTVEIKRTV 133

RESULT 11
US-10-697-995-11
Sequence 11, Application US/10697995
Publication No. US20050048572A1
GENERAL INFORMATION:
APPLICANT: Reilly, Dorothea
APPLICANT: Yaneura, Daniel G.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INCREASING ANTIBODY PRODUCTION
FILE REFERENCE: 11669.195USU1
CURRENT APPLICATION NUMBER: US/10/697, 995
CURRENT FILING DATE: 2003-10-30
PRIOR APPLICATION NUMBER: US 60/422,952
PRIOR FILING DATE: 2002-10-31
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 11
LENGTH: 237
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Anti-VEGF light chain
US-10-697-995-11

Query Match 100.0%; Score 575; DB 17; Length 237;
Best Local Similarity 100.0%; Pred. No. 3.7e-40;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTSPSSLSASVGDRTVITCSASODISNLYNMYQOKPGKAPKVLIFTSSLSHGVPS 60
DB 24 DIQLTSPSSLSASVGDRTVITCSASODISNLYNMYQOKPGKAPKVLIFTSSLSHGVPS 83
QY 61 RFGSGSGTDFLTITSLQPEDPATYCCQYSTVPMTFGGTVEIKRTV 110
DB 84 RFGSGSGTDFLTITSLQPEDPATYCCQYSTVPMTFGGTVEIKRTV 133

RESULT 12
US-10-234-671-8
Sequence 8, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997

ATTORNEY/AGENT INFORMATION:

NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-10-234-671-8

Query Match 99.7%; Score 573; DB 14; Length 110;
Best Local Similarity 99.1%; Pred. No. 2.6e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTSPSSLSASVGDRTVITCSASODISNLYNMYQOKPGKAPKVLIFTSSLSHGVPS 60
DB 1 DIQLTSPSSLSASVGDRTVITCSASODISNLYNMYQOKPGKAPKVLIFTSSLSHGVPS 60
QY 61 RFGSGSGTDFLTITSLQPEDPATYCCQYSTVPMTFGGTVEIKRTV 110
DB 61 RFGSGSGTDFLTITSLQPEDPATYCCQYSTVPMTFGGTVEIKRTV 110

RESULT 13

US-10-624-153-94
Sequence 94, Application US/10624153
Publication No. US20040086502A1
GENERAL INFORMATION:

APPLICANT: CHEN, YVONNE M.
APPLICANT: LOWMAN, HENRY B.
APPLICANT: MULLER, YVES
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469RIC1

CURRENT APPLICATION NUMBER: US/10/624,153
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: US 09/440,781
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: US 60/108,945
PRIOR FILING DATE: 1998-11-18
NUMBER OF SEQ ID NOS: 99

SEQ ID NO 94

LENGTH: 110

TYPE: PRT

ORGANISM: artificial sequence

FEATURE:

OTHER INFORMATION: sequence is synthesized

NAME/KEY: artificial

LOCATION: 1-110

OTHER INFORMATION: humanized antibody light chain variable domain

US-10-624-153-94

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: March 14, 2005, 20:39:29 / Search time 16.6447 Seconds
(without alignments)
635.867 Million cell updates/sec

Title: US-09-723-752b-115
Perfect score: 575
Sequence: 1 DIQLTQSPSSLSASVGDRTV.....YSTVPWTFGGTVEIKRTV 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	510	88.7	127	2 S40367	Ig kappa chain V-J
2	487	84.7	108	1 K1HUNU	Ig kappa chain V-I
3	483	84.0	125	2 S40333	Ig kappa chain V-J
4	482	83.8	123	2 S40331	Ig kappa chain - h
5	481	83.7	108	2 S49047	Ig kappa chain V r
6	479	83.3	131	2 S40352	Ig kappa chain V-J
7	479	83.3	108	2 S44132	Ig kappa chain V r
8	477	83.3	109	2 S31998	Ig kappa chain - h
9	477	83.0	107	2 S36264	Ig lambda chain V
10	477	83.0	129	2 S52789	Ig kappa chain V r
11	473.5	82.3	124	2 S40336	Ig kappa chain V-J
12	473	82.3	129	2 S40359	Ig kappa chain - h
13	471	81.9	108	1 K1HUNU	Ig kappa chain V-I
14	470	81.7	108	2 S19674	Ig kappa chain V r
15	470	81.7	132	2 S40334	Ig kappa chain - h
16	469	81.6	108	1 K1HUNE	Ig kappa chain V-I
17	469	81.6	119	2 S31981	Ig kappa chain - h
18	469	81.6	111	2 A38740	Ig kappa chain V r
19	469	81.6	125	2 S40349	Ig kappa chain V-J
20	467	81.6	110	2 S44118	Ig kappa chain V-J
21	466	81.0	108	1 K1HUNE	Ig kappa chain V-I
22	466	81.0	139	2 S40365	Ig kappa chain - h
23	465.5	81.0	107	2 S36275	Ig lambda chain V
24	464	80.7	108	1 K1HUNG	Ig kappa chain V-I
25	464	80.7	108	1 K1HUNB	Ig kappa chain V-I
26	463	80.5	108	2 S40360	Ig kappa chain - h
27	463	80.5	130	2 S40366	Ig kappa chain - h
28	462	80.3	125	2 S40316	Ig kappa chain - h
29	461	80.2	108	2 I39154	Ig kappa chain (BR

30	461	80.2	111	2 E38740	Ig kappa chain V r
31	461	80.2	122	2 S40370	Ig kappa chain - h
32	459	79.8	108	1 K1HUNE	Ig kappa chain V-I
33	459	79.8	111	2 C38740	Ig kappa chain V r
34	459	79.8	122	2 S40314	Ig kappa chain - h
35	459	79.8	129	2 S52793	Ig kappa chain V r
36	459	79.8	129	2 S52793	Ig kappa chain pre
37	459	79.8	135	2 S24320	anti-HIV1 envelope
38	458	79.7	107	2 I69017	Ig kappa chain - h
39	457.5	79.6	125	2 S40315	Ig lambda chain V
40	457	79.5	107	2 S36269	Ig kappa chain V-J
41	457	79.5	117	2 S46371	Ig kappa chain V-I
42	457	79.5	129	1 K1HUNK	Ig kappa chain pre
43	456	79.3	111	2 G38740	Ig kappa chain V r
44	456	79.3	117	2 S46376	Ig kappa chain V-J
45	456	79.3	128	2 S46372	Ig light chain var

ALIGNMENTS

```

RESULT 1
S40367
Ig kappa chain V-J-C region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40367
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40367
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-127 <RLS>
A/Cross-references: EMBL:X72477
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/33-107/Domain: immunoglobulin homology <IMM>

Query Match      88.7%; Score 510; DB 2; Length 127;
Best Local Similarity 89.1%; Pred. No. 5.3e-38;
Matches 98; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVTTTCSASQDSINYNINWQKRGKAPKVLIVFTSLHSGVPS 60
Db 18 DIQMTQSPSSLSASVGDRTVITCRASQISINYNWQKRGKAPKLVIAASLQSGVPS 77
QY 61 RFSGSGSGTDFTLTISLQPEDPATYCCOYSTVPWTFGGTVEIKRTV 110
Db 78 RFSGSGSGTDFTLTISLQPEDPATYCCOQSYNTPMTFGGTVEIKRTV 127

RESULT 2
K1HUNU
Ig kappa chain V-I region (Au) - human
C/Species: Homo sapiens (man)
C/Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C/Accession: A91653; A01862; S02573
R/Schlehl, H.; Hylleberg, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A/Title: Die Primärstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Su
A/Reference number: A91653; MUID:72189444; PMID:5028201
A/Accession: A91653
A/Molecule type: protein
A/Residues: 1-108 <SCH>
A/Cross-references: UNIPROT:P01594
A/Note: the C region of this chain has the Inv (3) marker
R/Fellhammer, H.; Schiffer, M.; Bep, O.; Colman, P.M.; Lettman, E.E.; Schwager, P.; Ste
Biophys. Struct. Mech. 1, 139-146, 1975
A/Title: The structure determination of the variable portion of the Bence-Jones protein
A/Reference number: A90729; MUID:77022433; PMID:1234024
A/Contents: annotation; X-ray crystallography

```

A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 15131 <K1.E>
A:Cross-references: EMBL:X72462; NID:g441392; PIDD:CAAS130.1; PIDD:g441392
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 83.7%; Score 481; DB 2; Length 131;
Best Local Similarity 84.5%; Pred. No. 1.9e-35;
Matches 93; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQLTGSPSSLSASVGDRTVITTCASODISNYLNMWYQKRGKAPKVLITFTSSLSHGVS 60
|||
DB 21 DIQMTGSPSSLSASVGNRRVITTCRASGGSINYLAWYQKRGKAPKVLITFTSSLSHGVS 80
QY 61 RFGSGSGTDFTLTISLQPEDPATYTCQOYSTVPMTFGGGTKEIKR 110
|||
DB 81 RFGSGSGTDFTLTISLQPEDPATYTCQKXNSVPRFPGGTKEIKR 130

RESULT 7

844122
Ig kappa chain V region - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001

C/Accession: S44122

R.Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, P.K.
submitted to the EMBL Data Library, March 1994

A/Description: T10cytic vaccination against human B-cell lymphoma: rescue of variable

A/Reference number: S44105

A/Accession: S44122

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-108 <HAM>

A/Cross-references: EMBL:231390; NID:g472976; PID:CAA83265.1; PID:g940533

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 479; DB 2; Length 108;
Best Local Similarity 86.1%; Pred. No. 2.4e-35;
Matches 93; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQLTGSPSSLSASVGDRTVITTCASODISNYLNMWYQKRGKAPKVLITFTSSLSHGVS 60
|||
DB 1 DIQMTGSPSSLSASVGNRRVITTCRASGGSINYLAWYQKRGKAPKVLITFTSSLSHGVS 60
QY 61 RFGSGSGTDFTLTISLQPEDPATYTCQOYSTVPMTFGGGTKEIKR 108
|||
DB 61 RFGSGSGTDFTLTISLQPEDPATYTCQOYSTVPMTFGGGTKEIKR 108

RESULT 8

S31998
Ig kappa chain - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000

C/Accession: S31998

R.Porciatano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992

A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as

A/Reference number: S31977

A/Accession: S31998

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-109 <POR>

A/Cross-references: EMBL:215081; NID:g38501; PID:CAA78790.1; PID:g38502

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 479; DB 2; Length 109;
Best Local Similarity 84.4%; Pred. No. 2.4e-35;
Matches 92; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQLTGSPSSLSASVGDRTVITTCASODISNYLNMWYQKRGKAPKVLITFTSSLSHGVS 60
|||
DB 1 ELVMTGSPSSLSASVGNRRVITTCRASGGSINYLAWYQKRGKAPKVLITFTSSLSHGVS 60

QY 61 RFGSGSGTDFTLTISLQPEDPATYTCQOYSTVPMTFGGGTKEIKR 109
|||
DB 61 RFGSGSGTDFTLTISLQPEDPATYTCQOYSTVPMTFGGGTKEIKR 109

RESULT 9

S36264
Ig lambda chain V region (clone alpha-CRA4-8A) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000

C/Accession: S36264

R.Griffiths, A.D.; Malmyr, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993

A/Title: Human anti-self antibodies with high specificity from phage display libraries.

A/Reference number: S36256; M0ID:93178448; PMID:7679990

A/Accession: S36264

A/Status: preliminary; nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-107 <GRI>

A/Cross-references: EMBL:218845; NID:g33426; PID:CAA79297.1; PID:g939919

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 477; DB 2; Length 107;
Best Local Similarity 86.9%; Pred. No. 3.5e-35;
Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQLTGSPSSLSASVGDRTVITTCASODISNYLNMWYQKRGKAPKVLITFTSSLSHGVS 60
|||
DB 1 ELVLTGSPSSLSASVGNRRVITTCRASGGSINYLAWYQKRGKAPKVLITFTSSLSHGVS 60
QY 61 RFGSGSGTDFTLTISLQPEDPATYTCQOYSTVPMTFGGGTKEIKR 107
|||
DB 61 RFGSGSGTDFTLTISLQPEDPATYTCQOYSTVPMTFGGGTKEIKR 107

RESULT 10

S52789
Ig kappa chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C/Accession: S52789

R.Rocca, A.; Khamilchi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoy, L.; Deret,
submitted to the EMBL Data Library, March 1995

A/Description: Light chain V region gene usage restriction and peculiarities in myeloma.

A/Reference number: S52789

A/Accession: S52789

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-129 <ROC>

A/Cross-references: EMBL:X85995; NID:g758589; PID:CAA59987.1; PID:g758589

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/38-112/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 477; DB 2; Length 129;
Best Local Similarity 85.0%; Pred. No. 4.3e-35;
Matches 91; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQLTGSPSSLSASVGDRTVITTCASODISNYLNMWYQKRGKAPKVLITFTSSLSHGVS 60
|||
DB 23 DIQMTGSPSSLSASVGNRRVITTCASODISNYLNMWYQKRGKAPKVLITFTSSLSHGVS 82
QY 61 RFGSGSGTDFTLTISLQPEDPATYTCQOYSTVPMTFGGGTKEIKR 107
|||
DB 83 RFGSGSGTDFTLTISLQPEDPATYTCQOYSTVPMTFGGGTKEIKR 129

RESULT 11

S40336

Ig kappa chain V-J region - human

C/Species: Homo sapiens (man)

C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40336
 R/Klein, R.; Jaenichen, H. G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40332; MUID:94080891; PMID:8258341
 A/Accession: S40336
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-124 <KDE>
 A/Cross-references: EMBL:X72446; NID:G441360; PIDN:CAAS114.1; PID:G441361
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/31-105/Domain: immunoglobulin homology <IMM>

Query Match 82.3%; Score 473.5; DB 2; Length 124;
 Best Local Similarity 85.3%; Pred. No. 8.3e-35;
 Matches 93; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGRVITTCASQDISNYLNMWYQKPGKAPKVLITYFTSSLHSGVPS 60
 |||||
 Db 16 DIQLTQSPSSLSASVGRVITTCRASQGISYLAWYQKPGKAPKVLITYAASLQSGVPS 75
 |||||

Qy 61 RFGSGSGTDFTLTITSLQPEDFATYYCOQYSTV-PWTFGGGTKEIKR 108
 |||||
 Db 76 RFGSGSGTDFTLTITSLQPEDFATYYCQQLNTYPPWTFGGGTKEIKR 124
 |||||

RESULT 12

S40369

Ig kappa chain - human
 C/Species: Homo sapiens (man)
 C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40369
 R/Klein, R.; Jaenichen, H. G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341
 A/Accession: S40369
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-129 <KDE>
 A/Cross-references: EMBL:X72479; NID:G441426; PIDN:CAAS114.1; PID:G441427
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/37-111/Domain: immunoglobulin homology <IMM>

Query Match 82.3%; Score 473; DB 2; Length 129;
 Best Local Similarity 84.3%; Pred. No. 9.6e-35;
 Matches 91; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGRVITTCASQDISNYLNMWYQKPGKAPKVLITYFTSSLHSGVPS 60
 |||||
 Db 22 DIQLTQSPSSLSASVGRVITTCRASVHISNHLVWFQKPGKAPKVLITYAASLQSGVPS 81
 |||||

Qy 61 RFGSGSGTDFTLTITSLQPEDFATYYCOQYSTV-PWTFGGGTKEIKR 108
 |||||
 Db 82 RFGSGSGTDFTLTITSLQPEDFATYYCQQYNSTYPPWTFGGGTKEIKR 129
 |||||

RESULT 13

K1RHU

Ig kappa chain V-I region (Hau) - human
 C/Species: Homo sapiens (man)
 C/Date: 24-Apr-1994 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
 C/Accession: A01868; S02574
 R/Matambes, S.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 351, 1291-1295, 1970
 A/Title: The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subg
 A/Reference number: A01868; MUID:71032830; PMID:4097974
 A/Accession: A01868
 A/Molecule type: protein
 A/Residues: 1-108 <MAT>

A/Cross-references: UNIPROT:P01600
 A/Note: The C region of this chain has the Inv (3) marker
 R/Steiner, V.; Chang, J. Y.
 FEBS Lett. 222, 6-10, 1987
 A/Title: Chemical modification of the carboxyl groups of protein substrates enhances th
 A/Reference number: S02572; MUID:88005152; PMID:3115831
 A/Contents: annotation
 C/Comment: This is a Bence Jones protein.
 C/Genetics:
 A/Gene: GDB:IGKV1
 A/Cross-references: GDB:136264
 A/Map position: 2p12-2p12
 C/Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kai
 hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into 1
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/16-90/Domain: immunoglobulin homology <IMM>
 F/23-88/Domain: heterotetramer predicted

Query Match 81.9%; Score 471; DB 1; Length 108;
 Best Local Similarity 85.2%; Pred. No. 1.2e-34;
 Matches 92; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGRVITTCASQDISNYLNMWYQKPGKAPKVLITYFTSSLHSGVPS 60
 |||||
 Db 1 DIQLTQSPSSLSASVGRVITTCRASQGISYLAWYQKPGKAPKVLITYAASLQSGVPS 60
 |||||

Qy 61 RFGSGSGTDFTLTITSLQPEDFATYYCOQYSTV-PWTFGGGTKEIKR 108
 |||||
 Db 61 RFGSGSGTDFTLTITSLQPEDFATYYCQQNYTPWTFGGGTKEIKR 108
 |||||

RESULT 14

S19674

Ig kappa chain V region (clone alpha-TE19) - human
 C/Species: Homo sapiens (man)
 C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
 C/Accession: S19674
 R/Marks, J. D.; Hoogenboom, H. R.; Bonnett, T. P.; McCafferty, J.; Griffiths, A. D.; Winter, J. M.
 J. Mol. Biol. 222, 581-597, 1991
 A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on p
 A/Reference number: S19663; MUID:92085276; PMID:1748994
 A/Accession: S19674
 A/Molecule type: mRNA
 A/Residues: 1-108 <MKR>
 A/Cross-references: EMBL:X61642; NID:G37860; PIDN:CAAS3823.1; PID:G1335386
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.7%; Score 470; DB 2; Length 108;
 Best Local Similarity 84.3%; Pred. No. 1.5e-34;
 Matches 91; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGRVITTCASQDISNYLNMWYQKPGKAPKVLITYFTSSLHSGVPS 60
 |||||
 Db 1 EIVLTQSPSSLSASVGRVITTCASQDISNYLNMWYQKPGKAPKVLITYAASLQSGVPS 60
 |||||

Qy 61 RFGSGSGTDFTLTITSLQPEDFATYYCOQYSTV-PWTFGGGTKEIKR 108
 |||||
 Db 61 RFGSGSGTDFTLTITSLQPEDFATYYCQQNSRPLPFGGTKEIKR 108
 |||||

RESULT 15

S40334

Ig kappa chain - human
 C/Species: Homo sapiens (man)
 C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40334
 R/Klein, R.; Jaenichen, H. G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341

A/Accession: S40334
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-132 <KLB>
A/Cross-references: EMBL:X72444
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/37-111/Domain: immunoglobulin homology <IMM>

Query Match 81.7%; Score 470; DB 2; Length 132;
Best Local Similarity 80.9%; Pred. No. 1.8e-34;
Matches 89; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

Qy	1	DIQLTQSPSLASVGDRTITCSASQDISNYLNMVQOKPKAPKVLIIYFTSLHSGVPS	60
		: : : : : : : : :	
Db	22	DIQLTQSPSLASIGDRVTITCRASQINSYLAWYQOKPKAPKLLIYVASTLQSGVPS	81
		: : : : : : : : :	
Qy	61	RPSGSGSGTDFTLTISLQPEDPATYYCQXYSTVPTFGQGTKEIERTV	110
		: : : : : : : : :	
Db	82	RPSGSGSGTEFTLTISLQPEDPASYYCQPFNSYPFTFGGTKEIERTV	131
		: : : : : : : : :	

Search completed: March 14, 2005, 21:08:52
CDB time : 17.6447 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2005, 20:32:33 ; Search time 77.193 Seconds
(without alignments)
729.713 Million cell updates/sec

Title: US-09-723-752B-115

Perfect score: 575
Sequence: 1 DIQLTQSPSSLSASVGDRTV.....YSTVPMTFGQIKVEIKRTV 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : 1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	487	84.7	108	KV1B_HUMAN	P01594 homo sapien
2	485	84.3	108	Q9UL77	Q9UL77 homo sapien
3	483	84.0	236	Q6GMX9	Q6GMX9 homo sapien
4	482	83.8	236	Q6GMW1	Q6GMW1 homo sapien
5	481	83.7	236	Q7Z3Y4	Q7Z3Y4 homo sapien
6	474.5	82.5	107	Q96S89	Q96S89 homo sapien
7	474	82.4	236	Q6GMX8	Q6GMX8 homo sapien
8	471	81.9	108	KV1H_HUMAN	P01600 homo sapien
9	471	81.9	108	KV1Y_HUMAN	P01362 homo sapien
10	471	81.9	236	Q6GMX0	Q6GMX0 homo sapien
11	469	81.6	108	KV1R_HUMAN	P01610 homo sapien
12	466	81.0	108	Q9UL70	P01607 homo sapien
13	465	80.9	108	Q9UL70	P01607 homo sapien
14	465	80.9	236	Q6PIH7	Q6PIH7 homo sapien
15	464	80.7	108	KV1A_HUMAN	P01593 homo sapien
16	464	80.7	108	KV1V_HUMAN	P04430 homo sapien
17	462	80.3	234	Q7Z473	Q7Z473 homo sapien
18	459	79.8	108	KV1P_HUMAN	P01608 homo sapien
19	457	79.5	129	KV1W_HUMAN	P04431 homo sapien
20	455	79.1	108	KV1E_HUMAN	P01597 homo sapien
21	454.5	79.0	107	KV1D_HUMAN	P01596 homo sapien
22	454	79.0	108	KV1M_HUMAN	P01605 homo sapien
23	453	78.8	108	KV1K_HUMAN	P01603 homo sapien
24	452.5	78.7	107	Q9UL81	Q9UL81 homo sapien
25	452	78.6	244	Q65ZC8	Q65ZC8 homo sapien
26	449	78.1	108	KV1Q_HUMAN	P01609 homo sapien
27	448	77.9	108	KV1J_HUMAN	P01611 homo sapien
28	447	77.7	116	Q96PF6	Q96PF6 homo sapien
29	447	77.7	108	KV1N_HUMAN	P01606 homo sapien
30	446	77.6	108	KV1C_HUMAN	P01595 homo sapien
31	445	77.4	108	KV5J_MOUSE	P01643 mus musculu

32	445	77.4	236	2	Q6PI75	Q6PI75 homo sapien
33	445	77.4	240	2	Q65ZC9	Q65ZC9 homo sapien
34	443	77.0	108	1	KV1G_HUMAN	P01599 homo sapien
35	439	76.3	108	1	KV1F_HUMAN	P01598 homo sapien
36	439	76.3	108	1	KV1L_HUMAN	P01604 homo sapien
37	439	76.3	108	2	Q9UL79	Q9UL79 homo sapien
38	438	76.2	236	2	Q6PIH4	Q6PIH4 homo sapien
39	428	74.4	108	1	KV5K_MOUSE	P01647 mus musculu
40	428	74.4	108	1	KV5N_MOUSE	P01645 mus musculu
41	426	74.1	108	1	KV5L_MOUSE	P01646 mus musculu
42	426	74.1	108	1	KV5M_MOUSE	P01646 mus musculu
43	425	73.9	108	1	KV5O_MOUSE	P01642 mus musculu
44	424.5	73.8	109	1	KV1T_HUMAN	P01612 homo sapien
45	422	73.4	108	1	KV5U_MOUSE	P01646 mus musculu

ALIGNMENTS

RESULT 1
ID KV1B_HUMAN STANDARD, PRT, 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-1 region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=77022433; PubMed=1234024;
RA Fehlgammer H., Schliffer M., Bpp O., Colman P.M., Lattman B.E.,
RA Schweiger P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the Bence-
RT Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -1- MISCELLANEOUS: The structure of the V region was determined by
CC molecular replacement using the known structure of the V
CC region of the kappa chain RFI.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91653; KIHUAV.
DR PDB; 1JVS; X-ray; A=1-107.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGY_1.
DR PROSITE; PS50835; IG_LIKE_1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT STRAND 4 5

```
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 44 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 97 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E801187EB6FEFB9 CRC64;

Query Match 84.7%; Score 487; DB 1; Length 108;
Best Local Similarity 85.2%; Pred. No. 2,3e-42;
Matches 92; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

1 DIQITQSPSSLSASVGRVITTCASQDISNYLNMVQOKPGKAPKVLITYFTSSLSHGVP 60
1 DIQITQSPSSLSASVGRVITTCASQDISNYLNMVQOKPGKAPKVLITYFTSSLSHGVP 60
Db 1 DIQITQSPSSLSASVGRVITTCASQDISNYLNMVQOKPGKAPKVLITYFTSSLSHGVP 60
Qy 1 DIQITQSPSSLSASVGRVITTCASQDISNYLNMVQOKPGKAPKVLITYFTSSLSHGVP 60
Db 1 DIQITQSPSSLSASVGRVITTCASQDISNYLNMVQOKPGKAPKVLITYFTSSLSHGVP 60
Qy 61 RFSGSGSGTDFTLTISLQPEDFATYVCOQYSTVPWTFGQTKVEIKR 108
61 RFSGSGSGTDFTLTISLQPEDFATYVCOQYSTVPWTFGQTKVEIKR 108
Db 61 RFSGSGSGTDFTLTISLQPEDFATYVCOQYSTVPWTFGQTKVEIKR 108

RESULT 2
ID Q9UL77 PRELIMINARY; PRT: 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalle N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus ";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AA056273.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSSP; P01607; 1BWM.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 84.3%; Score 485; DB 2; Length 108;
Best Local Similarity 86.1%; Pred. No. 3,8e-42;
Matches 93; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

1 DIQITQSPSSLSASVGRVITTCASQDISNYLNMVQOKPGKAPKVLITYFTSSLSHGVP 60
1 DIQITQSPSSLSASVGRVITTCASQDISNYLNMVQOKPGKAPKVLITYFTSSLSHGVP 60
Db 1 DIQITQSPSSLSASVGRVITTCASQDISNYLNMVQOKPGKAPKVLITYFTSSLSHGVP 60
Qy 1 DIQITQSPSSLSASVGRVITTCASQDISNYLNMVQOKPGKAPKVLITYFTSSLSHGVP 60
Db 1 DIQITQSPSSLSASVGRVITTCASQDISNYLNMVQOKPGKAPKVLITYFTSSLSHGVP 60
Qy 61 RFSGSGSGTDFTLTISLQPEDFATYVCOQYSTVPWTFGQTKVEIKR 110
61 RFSGSGSGTDFTLTISLQPEDFATYVCOQYSTVPWTFGQTKVEIKR 110
```

```
Db 1 DIQITQSPSSLSASVGRVITTCASQDISNYLNMVQOKPGKAPKVLITYFTSSLSHGVP 60
Qy 61 RFSGSGSGTDFTLTISLQPEDFATYVCOQYSTVPWTFGQTKVEIKR 108
61 RFSGSGSGTDFTLTISLQPEDFATYVCOQYSTVPWTFGQTKVEIKR 108
Db 61 RFSGSGSGTDFTLTISLQPEDFATYVCOQYSTVPWTFGQTKVEIKR 108

RESULT 3
ID Q6GMX9 PRELIMINARY; PRT: 236 AA.
AC Q6GMX9;
DT 05-JUN-2004 (TrEMBLrel. 27, Created)
DT 05-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhac N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshibuyuki S., Carninci P., Prange C.,
RA Rana S.S., Loguclano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Gay L.J., Holik S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Holik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scheraga A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences ";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073763; AAHT3763.1; -.
DR InterPro; IPR003599; IG_1like.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-sect; 1.
DR Pfam; PF00047; Ig; 2.
DR Pfam; SM00409; Ig; 2.
DR SMART; SM00407; IGV_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25924 MW; FBE2093DC560CF7 CRC64;

Query Match 84.0%; Score 483; DB 2; Length 236;
Best Local Similarity 85.5%; Pred. No. 1,5e-47;
Matches 94; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

1 DIQITQSPSSLSASVGRVITTCASQDISNYLNMVQOKPGKAPKVLITYFTSSLSHGVP 60
1 DIQITQSPSSLSASVGRVITTCASQDISNYLNMVQOKPGKAPKVLITYFTSSLSHGVP 60
Db 23 DIQITQSPSSLSASVGRVITTCASQDISNYLNMVQOKPGKAPKVLITYFTSSLSHGVP 82
61 RFSGSGSGTDFTLTISLQPEDFATYVCOQYSTVPWTFGQTKVEIKR 110
```

DB 83 RFGSGSGTDFLTITSLQPEDFATYCCQYKSTVMTFGQTKVEIKRTV 132

RESULT 4
ID 06GMM1 PRELIMINARY; PRT; 236 AA.
AC 06GMM1; 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX MEDLINE=22388257; Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywiński M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Spleen;
RC Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -
DR InterPro; IPR003599; IG_c1.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003066; IG_MHC.
DR Pfam; PF07654; C1-sec; 1.
DR Pfam; PF00047; IG_2.
DR SMART; SM00409; IG_2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PSS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KM Hypothetical protein.
SQ SEQUENCE 236 AA; 25751 MW; 58FBEA087AFAC437 CRC64;
Query Match 83.8%; Score 482; DB 2; Length 236;
Best Local Similarity 87.2%; Pred. No. 1.9e-41;
Matches 95; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

Qy 2 IQLTQSSSLASVGDRTVITTCASODISNLYLAWYQKRGKAPKYLITFTSSLSHGVPSR 61
Db 24 IQMTQSSSLASVGDRTVITTCASODISNLYLAWYQKRGKAPKYLITFTSSLSHGVPSR 83
Qy 62 FSGSGSGTDFLTITSLQPEDFATYCCQYKSTVMTFGQTKVEIKRTV 110
Db 84 FSGSGSGTDFLTITSLQPEDFATYCCQYKSTVMTFGQTKVEIKRTV 132

RESULT 5
ID 0723Y4 PRELIMINARY; PRT; 236 AA.
AC 0723Y4; 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywiński M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Skeletal Muscle;
RC Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AAH05332.1; -
DR HSP; P01834; 1HEZ.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003066; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-sec; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PSS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KM Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7FBFB4BD23084BC6 CRC64;

Qy 1 DIQLTQSSSLASVGDRTVITTCASODISNLYLAWYQKRGKAPKYLITFTSSLSHGVPS 60
Db 23 DIQLTQSSSLASVGDRTVITTCASODISNLYLAWYQKRGKAPKYLITFTSSLSHGVPS 82
Qy 61 RFGSGSGTDFLTITSLQPEDFATYCCQYKSTVMTFGQTKVEIKRTV 110
Db 83 RFGSGSGTDFLTITSLQPEDFATYCCQYKSTVMTFGQTKVEIKRTV 132
RESULT 6
ID 096SA9 PRELIMINARY; PRT; 107 AA.
AC 096SA9; 01-DEC-2001 (TReMBLrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, last annotation update)
 DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
 DE variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxId=9606;
 RX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=98375893; PubMed=9712075;
 RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
 RT "Molecular analysis of polyclonal monoclonal antibodies from
 rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
 antibody V region genes.";
 RT J. Immunol. 161:2020-2031(1998).
 RL EMBL; U96396; AAB6785.1; -;
 DR PIR; B49047; B49047.
 DR PIR; PH0867; PH0867.
 DR PIR; S16840; S16840.
 DR PIR; S31977; S31977.
 DR PIR; S34083; S34083.
 DR PIR; S34086; S34086.
 DR HSP; P01607; 1BMW.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003596; IG_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1 107
 PT 107
 SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 82.5%; Score 474.5; DB 2; Length 107;
 Best Local Similarity 88.1%; Pred. No. 4.5e-41;
 Matches 96; Conservative 4; Mismatches 6; Indels 3; Gaps 2;
 QY 1 DIQTQSPSSLSASVGRVITTCASQDISNYLNMVQKPKGAPKVLITYFTSSLSHGVS 60
 DB 1 DIQTQSPSSLSASVGRVITTCASQDISNYLNMVQKPKGAPKVLITYFTSSLSHGVS 60
 QY 61 RFSGSGSGTDFTLTITSLQPEDPATYCCQ-YSTVPWTFGGCTKVEIKR 108
 DB 61 RFSGSGSGTDFTLTITSLQPEDPATYCCQYSHSPFTFGGTVDIKRTV 132

RESULT 7
 Q6GMX8 PRELIMINARY; PRT; 236 AA.
 AC Q6GMX8;
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxId=9606;
 RX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Steplowitz M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Cantini P., Pange C.,
 RA Raba S.S., Lequellano N.A., Peters G.J., Abrahamson R.D., Mullaly S.J.,
 RA Boeck S.A., McBreen P.J., McKernan K.J., Malek J.A., Gunatirane P.H.,
 RA Richards S., Morley C.C., Hale S., Garcia A.W., Gay L.J., Huij S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Small D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Straube R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073764; AAH73764.1; -;
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003066; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; C1-sec; 1.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG_C1; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 25707 MW; 4FCBE14B6559EFC9 CRC64;

Query Match 82.4%; Score 474; DB 2; Length 236;
 Best Local Similarity 83.6%; Pred. No. 1.3e-40;
 Matches 92; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
 QY 1 DIQTQSPSSLSASVGRVITTCASQDISNYLNMVQKPKGAPKVLITYFTSSLSHGVS 60
 DB 23 DIQTQSPSSLSASVGRVITTCASQDISNYLNMVQKPKGAPKVLITYFTSSLSHGVS 82
 QY 61 RFSGSGSGTDFTLTITSLQPEDPATYCCQYSHSPFTFGGTVDIKRTV 110
 DB 83 RFSGSGSGTDFTLTITSLQPEDPATYCCQYSHSPFTFGGTVDIKRTV 132

RESULT 8
 KV1H_HUMAN STANDARD; PRT; 108 AA.
 ID KV1H_HUMAN
 AC P01600;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig kappa chain V-I region Hu.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE
 RC MEDLINE=71032830; PubMed=4097974;
 RA Watanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
 RT chain of subgroup I (Bence-Jones Protein Hu): subdivision within
 RT subgroup.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A01688; K1H0H0.
 DR PDB; 1F6L; X-ray; L=1-108.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0005855; P:immune response; NAS.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IGV; 1.
 DR SMART; SM00406; IGV; 1.

DR PROSITE; PSS0835; IG LIKE; 1.
 KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
 KM Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Complementarity-determining-2.
 FT DOMAIN 50 56 Complementarity-determining-3.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Framework-4.
 FT DISULFID 98 107 By similarity.
 FT NON TER 23 88
 SO SEQUENCE 108 AA; 11671 MM; 08D3A6160DB0618 CRC64;
 Query Match 81.9%; Score 471; DB 1; Length 108;
 Best Local Similarity 85.2%; Pred. No. 1e-40;
 Matches 92; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
 QY 1 DIQLTQSPSSLSASVGDRTITCSASODISNLYMWYQKRGKAPKLYIFTSLSHGVP 60
 DB 1 DIQMTQSPSSLSASVGDRTITCRASQISSTYSWYQKRGKAPQVLYIYASSLPSCVPS 60
 QY 61 RFSGSGSGTDFLTITSLQPEDPATYTCQOYSTVPTFGGTVEIKR 108
 DB 61 RFSGSGSGTDFLTITSLQPEDPATYTCQOYSTVPTFGGTVEIKR 108
 RESULT 9
 ID KVLV HUMAN STANDARD; PRT; 108 AA.
 AC P80362;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig kappa chain V-J region MAT.
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=95086080; PubMed=7993911;
 RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
 RA Solomon A., Stevens F.J., Schiffer M.;
 RT "Comparison of crystal structures of two homologous proteins:
 RT structural origin of altered domain interactions in immunoglobulin
 RT light-chain dimers.";
 RT J. Biochem. 147:185-193(1991).
 RL J. Mol. Biol. 147:185-193(1991).
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PDB; 1WTU; X-ray; A/B=1-108.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; Ig_1.
 DR PROSITE; PSS0835; IG LIKE; 1.
 KM 3D-structure; Bence-Jones protein; Direct protein sequencing;
 KM Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Complementarity-determining-2.
 FT DOMAIN 50 56 Complementarity-determining-3.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Framework-4.

FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 107 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT CONFLICT 30 31 TN -> SD (in Ref. 2).
 FT STRAND 4 7
 FT STRAND 10 13
 FT STRAND 15 16
 FT STRAND 19 25
 FT STRAND 30 31
 FT STRAND 33 38
 FT STRAND 40 41
 FT STRAND 45 49
 FT STRAND 50 52
 FT STRAND 53 54
 FT STRAND 56 57
 FT STRAND 60 61
 FT STRAND 62 67
 FT STRAND 68 69
 FT STRAND 70 75
 FT HELIX 80 82
 FT STRAND 84 90
 FT STRAND 98 98
 FT STRAND 102 106
 FT NON TER 108 108
 SO SEQUENCE 108 AA; 11737 MM; D9D941B3F0FAE697 CRC64;
 Query Match 81.9%; Score 471; DB 1; Length 108;
 Best Local Similarity 82.4%; Pred. No. 1e-40;
 Matches 89; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
 QY 1 DIQLTQSPSSLSASVGDRTITCSASODISNLYMWYQKRGKAPKLYIFTSLSHGVP 60
 DB 1 DIQMTQSPSSLSASVGDRTITCRASQISSTYSWYQKRGKAPQVLYIYASSLPSCVPS 60
 QY 61 RFSGSGSGTDFLTITSLQPEDPATYTCQOYSTVPTFGGTVEIKR 108
 DB 61 RFSGSGSGTDFLTITSLQPEDPATYTCQOYSTVPTFGGTVEIKR 108
 RESULT 10
 ID O6GKX0 PRELIMINARY; PRT; 236 AA.
 AC O6GKX0;
 DT 05-JUL-2004 (TEMBLrel. 27, Created)
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Splice;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Heien N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Datchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schneetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tohilyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters E.J., Abramson R.D., Mullaly S.J.,
 RA Bosek S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muray D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Rhee J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strassberg R;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC073775; AAH73775.1; -.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-sec; 1.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KM Hypothetical protein.
 SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E2B8F CRC64;

Query March 81.9%; Score 471; DB 2; Length 236;
 Best Local Similarity 82.7%; Pred. No. 2.6e-40;
 Matches 91; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRVTITCSASQDISNYLNMVYQOKPKAPKVLITYFTSSLSHGVS 60
 DB 23 DIQMTQSPSSLSASVGDRVTITCRASQININNYLNMVYQOKPKAPKVLITYFTSSLSHGVS 82

QY 61 RFSGSGSGTDFTLTISLQPEDFATYVCOQYSTVPMWFGGTVKIKETV 110
 DB 83 RFSGSGSGTDFTLTISLQPEDFATYVCOQSYNIFLTFGGTVKIKETV 132

RESULT 11
 ID_KV10_HUMAN STANDARD; PRT; 108 AA.
 AC P01610;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE IG kappa chain V-I region WEA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=83273707; PubMed=6410398;
 RA Goni F., Frangione B.;
 RT "Antio acid sequence of the Fv region of a human monoclonal IGM
 (protein WEA) with antibody activity against 3,4-pyruvylated galactose
 in Klebsiella polysaccharides K30 and K33.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
 CC -1- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
 against 3,4-pyruvylated galactose and isolated from a patient with
 Waldenstrom's macroglobulinemia.
 DR HSSP; A01876; KIHUME.
 DR PIR; A01876; KIHUME.
 DR HSSP; A01876; KIHUME.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KM Direct protein sequencing; Immunoglobulin V region;
 KW Monoclonal antibody.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.

FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 107 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query March 81.6%; Score 469; DB 1; Length 108;
 Best Local Similarity 83.3%; Pred. No. 1.7e-40;
 Matches 90; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRVTITCSASQDISNYLNMVYQOKPKAPKVLITYFTSSLSHGVS 60
 DB 1 DIQMTQSPSSLSASVGDRVTITCRASQININNYLNMVYQOKPKAPKVLITYFTSSLSHGVS 60

QY 61 RFSGSGSGTDFTLTISLQPEDFATYVCOQYSTVPMWFGGTVKIKETV 108
 DB 61 RFSGSGSGTDFTLTISLQPEDFATYVCOQSYNIFLTFGGTVKIKETV 108

RESULT 12
 ID_KV10_HUMAN STANDARD; PRT; 108 AA.
 AC P01607;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE IG kappa chain V-I region Rel.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76033758; PubMed=809329;
 RA Palm W., Hilschmann N.;
 RT "The primary structure of a crystalline monoclonal immunoglobulin
 kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation
 and characterization of the tryptic peptides; the complete amino acid
 sequence of the protein; a contribution to the elucidation of the
 three-dimensional structure of antibodies, in particular their
 combining site.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=76039968; PubMed=1182131;
 RA Bep O., Iatman B.E., Schiffer M., Huber R., Palm W.;
 RT "The molecular structure of a dimer composed of the variable portions
 of the Bence-Jones protein RFI refined at 2.0-A resolution.";
 RL Biochemistry 14:4943-4952(1975).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
 marker.
 DR -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A9163; KIHURE.
 DR PDB; 1AR2; X-ray; @=1-107.
 DR PDB; 1BMW; X-ray; A/B=1-107.
 DR PDB; 1REI; X-ray; A/B=1-107.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KM 3D-structure; Bence-Jones protein; Direct protein sequencing;
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.


```
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88
FT STRAND 4 7
FT TURN 10 13
FT TURN 15 16
FT TURN 19 25
FT TURN 30 31
FT TURN 33 38
FT STRAND 40 41
FT TURN 45 49
FT STRAND 50 52
FT TURN 53 54
FT STRAND 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 84 90
FT STRAND 97 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A.CRC64;

Query Match 81.0%; Score 466; DB 1; Length 108;
Best Local Similarity 80.6%; Pred. No. 3,4e-40;
Matches 87; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Cy 1 DIDLQSPSSLSASVGDVRVITTCASODISNYLNMWQKPKAPKVLITYFTSSLHSGVPS 60
   1 DIDLQSPSSLSASVGDVRVITTCASODISNYLNMWQKPKAPKVLITYFTSSLHSGVPS 60
Db 1 DIDLQSPSSLSASVGDVRVITTCASODISNYLNMWQKPKAPKVLITYFTSSLHSGVPS 60
   1 DIDLQSPSSLSASVGDVRVITTCASODISNYLNMWQKPKAPKVLITYFTSSLHSGVPS 60
Cy 61 RFSSGSGTDFTLTISLPEDFATYYCQOYSTVPMPTFGQGTVEIKR 108
   61 RFSSGSGTDFTLTISLPEDFATYYCQOYSTVPMPTFGQGTVEIKR 108
Db 61 RFSSGSGTDFTLTISLPEDFATYYCQOYSTVPMPTFGQGTVEIKR 108
   61 RFSSGSGTDFTLTISLPEDFATYYCQOYSTVPMPTFGQGTVEIKR 108

RESULT 13
ID 09UL70 PRELIMINARY; PRT; 108 AA.
AC 09UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
   (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9827139; PubMed=9614934; DOI=10.1006/cln.1998.4531;
   Wu X., Liu B., Van der Werf P.L., Kalis N.N., Bertney S.M.,
   Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus."
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL; AF035064; AAD56280.1; -.
DR PIR; PH0863; PH0863.
DR HSSP; P01607; 18MW.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IG_v.1.
DR PROSITE; PSS0835; IG-LIKE; 1.
FT NON_TER 108 108
FT SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37.CRC64;

Query Match 80.9%; Score 465; DB 2; Length 108;
Best Local Similarity 83.3%; Pred. No. 4,3e-40;
Matches 83; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
```

```
Matches 90; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Cy 1 DIDLQSPSSLSASVGDVRVITTCASODISNYLNMWQKPKAPKVLITYFTSSLHSGVPS 60
   1 DIDLQSPSSLSASVGDVRVITTCASODISNYLNMWQKPKAPKVLITYFTSSLHSGVPS 60
Db 1 DIDLQSPSSLSASVGDVRVITTCASODISNYLNMWQKPKAPKVLITYFTSSLHSGVPS 60
   1 DIDLQSPSSLSASVGDVRVITTCASODISNYLNMWQKPKAPKVLITYFTSSLHSGVPS 60
Cy 61 RFSSGSGTDFTLTISLPEDFATYYCQOYSTVPMPTFGQGTVEIKR 108
   61 RFSSGSGTDFTLTISLPEDFATYYCQOYSTVPMPTFGQGTVEIKR 108
Db 61 RFSSGSGTDFTLTISLPEDFATYYCQOYSTVPMPTFGQGTVEIKR 108
   61 RFSSGSGTDFTLTISLPEDFATYYCQOYSTVPMPTFGQGTVEIKR 108

RESULT 14
ID 06PIH7 PRELIMINARY; PRT; 236 AA.
AC 06PIH7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
   Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
   Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
   Altschul S.F., Zeeberg B., Burow K.H., Schaefer C.F., Bhat N.K.,
   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
   Diatchenko L., Marusina K., Farmer A.A., Rubin C.M., Hong L.,
   Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
   Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
   Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
   Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
   Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
   Krzywicki M.I., Skalka U., Smallos D.E., Schnerch A., Schein J.E.,
   Jones S.J., Warr M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung;
RA Straubeberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034141; AAH34141.1; -.
DR HSSP; P01607; 1AR2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-sect.1.
DR SMART; SM00409; IG_2.
DR SMART; SM00407; IGcl.1.
DR SMART; SM00406; IG_v.1.
DR PROSITE; PSS0835; IG-LIKE; 2.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F.CRC64;

Query Match 80.9%; Score 465; DB 2; Length 236;
Best Local Similarity 83.6%; Pred. No. 1,1e-39;
Matches 92; Conservative 6; Mismatches 12; Indels 0; Gaps 0;
```

```

Db      23 DIQLTQSPFSLASVGDRTITCRASQGISSTLAMYQKPKAPNLLIYASTLQSGVPS 82
QY      61 RFGSGSGCTDFTLTITSSLOPEDPATYCCQYSTVPWTFQGTKEIKRTV 110
Db      83 RFGSGSGCTEFTLTITSSLOPEDPATYCCQQLNSPPTFGGKTKEIKRTV 132

```

RESULT 15

```

KVIA_HUMAN          STANDARD;          PRT;          108 AA.
ID   P01593
AC   P01593
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-I region AG.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX   NCBI_TaxID=9606;
RX   MEDLINE=69234734; PubMed=4893682;
RA   Titeani K., Shinoda T., Putnam F.W.;
RT   "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT   complete sequence and the location of the disulfide bridges."
RL   J. Biol. Chem. 244:3550-3560(1969).
CC   -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR: A01861; KIHUAG.
DR   HSP: P01607; 1BWV.
DR   GO: GO:0005576; C:extracellular; NAS.
DR   GO: GO:0003823; F:antigen binding; NAS.
DR   GO: GO:0006955; P:immune response; NAS.
DR   InterPro: IPR007110; IG-like.
DR   InterPro: IPR003596; IG_V.
DR   Pfam: PF00047; Ig_1.
DR   SMART, SM00406; IGV_1.
DR   PROSITE, PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin V region.
FT   DOMAIN          1      23      Framework-1.
FT   DOMAIN          24      34      Complementarity-determining-1.
FT   DOMAIN          35      49      Framework-2.
FT   DOMAIN          50      56      Complementarity-determining-2.
FT   DOMAIN          57      88      Framework-3.
FT   DOMAIN          89      97      Framework-4.
FT   DOMAIN          98      107     Complementarity-determining-3.
FT   DISULFID        23      88
FT   NON_TER         108      108
SQ   SEQUENCE      108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

```

```

Query Match      80.7%; Score 464; DB 1; Length 108;
Best Local Similarity 81.5%; Pred. No. 5.5e-40;
Matches 88; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

```

```

QY      1 DIQLTQSPFSLASVGDRTITCRASQGISSTLAMYQKPKAPNLLIYFTSSLSHGVP 60
Db      1 DIQMTQSPFSLASVGDRTITCRASQGISSTLAMYQKPKAPNLLIYDASNLFTGVP 60
QY      61 RFGSGSGCTDFTLTITSSLOPEDPATYCCQYSTVPWTFQGTKEIKR 108
Db      61 RFGSGSGCTDFTLTITSSLOPEDPATYCCQYSTVPWTFQGTKEIKR 108

```

Search completed: March 14, 2005, 20:49:19
Job time : 78.193 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: March 14, 2005, 20:21:17 ; Search time 94.4518 Seconds
(without alignments)
483.186 Million cell updates/sec

Title: US-09-723-752b-116

Perfect score: 658
Sequence: 1 EVQLVESGGGLVQPGSSRLR.....YPRYTSTHMYFDVWGQCTL 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing filter 45 summaries

Database: A_Geneseq_16Dec04:*

1: geneseqp19808:.*
2: geneseqp19908:.*
3: geneseqp20008:.*
4: geneseqp20018:.*
5: geneseqp20028:.*
6: geneseqp20038:.*
7: geneseqp20038:.*
8: geneseqp20048:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	658	100.0	118	2	AAW70686 Anti-VEGF
2	658	100.0	118	2	AAW70688 Anti-VEGF
3	658	100.0	118	3	AAAB13385 Anti-VEGF
4	658	100.0	118	3	AAAB13384 Anti-VEGF
5	658	100.0	118	5	ABP61255 Humanised
6	658	100.0	118	5	ABP61257 Humanised
7	658	100.0	123	8	ADG31769 V(H) doma
8	658	100.0	254	5	ABP51953 Plasmid p
9	658	100.0	476	5	ABP81110 Anti-VEGF
10	658	100.0	476	8	ADG14129 Plasmid p
11	658	100.0	476	8	ADG90730 Anti-VEGF
12	654	99.4	117	7	ADP09953 Antibody
13	654	99.4	117	7	ADP10058 VEGF anti
14	649	98.6	118	2	AAW70682 Anti-VEGF
15	649	98.6	118	3	AAAB05900 F(ab)-12
16	649	98.6	118	3	AAAB13382 Anti-VEGF
17	649	98.6	118	5	ABP61251 Humanised
18	645	98.0	231	7	ADG26162 Anti-VEGF
19	640	97.3	118	2	AAW70684 Anti-VEGF
20	640	97.3	118	3	AAAB13383 Anti-VEGF
21	640	97.3	118	5	ABP61253 Humanised
22	640	97.3	231	7	ADG26158 Anti-VEGF
23	638	97.0	123	8	ADG31894 V(H) prot
24	635	96.5	118	2	AAW70678 Anti-VEGF
25	635	96.5	118	3	AAAB05899 Humanised

26	635	96.5	118	3	AAAB13381 F(ab)-12
27	635	96.5	118	3	AAAB13389 Anti-VEGF
28	635	96.5	118	5	ABP61247 Humanised
29	635	96.5	123	2	AAW70617 Anti-VEGF
30	635	96.5	123	5	ABP61186 Humanised
31	635	96.5	123	8	ADG31767 V(H) doma
32	635	96.5	123	8	ADG31780 V(H) doma
33	635	96.5	231	7	ADG26155 Parent an
34	635	96.5	476	8	ADG90736 Anti-VEGF
35	633	96.2	118	2	ADG31892 V(H) prot
36	631	95.9	118	2	AAW70680 Anti-VEGF
37	631	95.9	118	5	ABP61249 Humanised
38	629	95.6	123	5	AAW70697 Anti-VEGF
39	629	95.6	123	5	ABP61266 Humanised
40	629	95.6	123	8	ADG31895 Anti-VEGF
41	627.5	95.4	121	3	AAAB05902 F(ab)-12
42	627.5	95.4	121	3	AAAB13391 Anti-VEGF
43	625.5	95.1	234	7	ADG26161 Anti-VEGF
44	620.5	94.3	234	7	ADG26163 Anti-VEGF
45	618	93.9	123	2	AAW70626 Humanised

ALIGNMENTS

RESULT 1
AAW70686 standard; peptide; 118 AA.
XX
XX
AC AAW70686;
XX
XX
DT 27-JUN-1999 (first entry)
XX
XX
DE Anti-VEGF humanised antibody variable heavy domain of variant Y0313-1.
XX
XX Heavy variable domain; murine; humanised antibody;
XX anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
XX VEGF-induced angiogenesis; tumour; retinal disorder;
XX age-related macular degeneration; diabetic retinopathy;
XX rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
XX
XX Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
XX MO9845331-A2.
XX
XX 15-OCT-1998.
XX
XX 03-APR-1998; 98WO-US006604.
XX
XX 07-APR-1997; 97US-00833504.
XX
XX 06-AUG-1997; 97US-00908469.
XX
XX (GETH) GENENTECH INC.
XX
XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
PI WPI; 1998-568337/48.
XX
XX New humanised antibody with affinity for vascular endothelial growth
XX factor - for treatment of tumours, retinal disease and other angiogenic
XX states, also related nucleic acid, vectors and transformed cells.
XX
XX Example 3; Fig 10B; 100p; English.
XX
XX The present sequence represents a variable heavy domain of an affinity-
XX maturated anti-vascular endothelial growth factor (anti-VEGF) antibody
XX variant. The sequence is used in the course of the invention to produce
XX the humanised anti-VEGF antibody of the invention. The humanised
XX antibodies are used to inhibit VEGF-induced angiogenesis, particularly
XX for treating or preventing tumours (of any type) and retinal disorders
XX (e.g. age-related macular degeneration or diabetic retinopathy). They can

CC also be used to treat other conditions that involve angiogenesis, e.g.
 CC rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc
 XX
 SQ Sequence 118 AA;

Query Match 100.0%; Score 658; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 2,66-56;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVOPGSGLRISCAASGYDFTHYGMNWRQAPGKLEWVGINITYGSEPT 60
 DB 1 EVQLVESGGGLVOPGSGLRISCAASGYDFTHYGMNWRQAPGKLEWVGINITYGSEPT 60
 QY 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYRYGTSHWYFDWVGQGL 118
 DB 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYRYGTSHWYFDWVGQGL 118

RESULT 2

ID AAW70688 standard; peptide; 118 AA.
 XX AAW70688;

DT 27-JAN-1999 (first entry)
 XX
 DE Anti-VEGF humanised antibody variable heavy domain of variant Y0317.

KM Heavy variable domain; murine; humanised antibody;
 KM anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
 KM VEGF-induced angiogenesis; tumour; retinal disorder;
 KM age-related macular degeneration; diabetic retinopathy;
 KM rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.

PN W09845331-A2.

PD 15-OCT-1998.

PF 03-APR-1998; 98WO-US006604.

PR 07-APR-1997; 97US-00833504.

PR 06-AUG-1997; 97US-00908469.

XX (GETH) GENENTECH INC.

PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX WPI; 1998-568337/48.

PT New humanised antibody with affinity for vascular endothelial growth
 PT factor - for treatment of tumours, retinal disease and other angiogenic
 PT sites; also related nucleic acid, vectors and transformed cells.

XX Claim 25; Fig 10B; 100pp; English.

CC The present sequence represents a variable heavy domain of an affinity-
 CC matured anti-vascular endothelial growth factor (anti-VEGF) antibody
 CC variant. The sequence is used in the course of the invention to produce
 CC the humanised anti-VEGF antibody of the invention. The humanised
 CC antibodies are used to inhibit VEGF-induced angiogenesis, particularly
 CC for treating or preventing tumours (of any type) and retinal disorders
 CC (e.g. age-related macular degeneration or diabetic retinopathy). They can
 CC also be used to treat other conditions that involve angiogenesis, e.g.
 CC rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc

XX Sequence 118 AA;

Query Match 100.0%; Score 658; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 2,66-56;

Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVOPGSGLRISCAASGYDFTHYGMNWRQAPGKLEWVGINITYGSEPT 60
 DB 1 EVQLVESGGGLVOPGSGLRISCAASGYDFTHYGMNWRQAPGKLEWVGINITYGSEPT 60
 QY 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYRYGTSHWYFDWVGQGL 118
 DB 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYRYGTSHWYFDWVGQGL 118

RESULT 3

ID AAB13385 standard; protein; 118 AA.
 XX AAB13385;

DT 21-NOV-2000 (first entry)

XX Anti-VEGF antibody Y0317 heavy chain variable domain.

DE Y0317; vascular endothelial cell growth factor; VEGF; antibody;
 KM antiinflammatory; cerebroprotective; cytostatic; antirheumatic;
 KM antiarthritic; antipsoriatic; antiarteriosclerotic; antidiabetic;
 KM antithyroid; excessive neovascularisation; tumour; rheumatoid arthritis;
 KM psoriasis; atherosclerosis; diabetes; retinoid fibroplasia;
 KM neovascular glaucoma; haemangioma; thyroid hyperplasia; Grave's disease;
 KM tissue transplantation; inflammation; oedema; trauma;
 KM complementarity determining region; CDR.

XX Unidentified.

OS Key Location/Qualifiers
 FH Region 26..35
 FT /label= CDR-H1
 FT Region 50..66
 FT /label= CDR-H2
 FT Region 70..79
 FT /label= CDR-7
 FT Region 99..112
 FT /label= CDR-H3

XX W0200037502-A2.

XX 29-JUN-2000.

PF 09-DEC-1999; 99WO-US029475.

PR 22-DEC-1998; 98US-00218481.

XX (GETH) GENENTECH INC.

PI Van Bruggen N, Ferrara N;

XX WPI; 2000-442646/38.

PT Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis,
 PT diabetes and chronic inflammation in a mammal, comprises administering a
 PT human vascular endothelial cell growth factor antagonist.

XX Disclosure; Fig 14B; 60pp; English.

CC The present sequence is the heavy chain variable region of the affinity
 CC matured anti-vascular endothelial cell growth factor (anti-VEGF) antibody
 CC Y0317. Humanised Fab-12 and affinity matured anti-VEGF antibodies may
 CC be used to treat conditions characterised by undesirable excessive
 CC neovascularisation. Such conditions include tumours (especially solid
 CC ones), rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and
 CC other retinopathies, retinoid fibroplasia, age-related macular
 CC degeneration, neovascular glaucoma, haemangioma, thyroid hyperplasia
 CC (including Grave's disease), corneal and other tissue transplantation,
 CC and chronic inflammation. Oedemas associated with tumours, strokes and
 CC head trauma, and aetiologies associated with malignancies, meig's syndrome,

CC lung inflammation, nephrotic syndrome, pericardial effusion and pleural
CC effusion, may also be treated. Monoclonal antibodies are generated in
CC hybridoma cells and those with affinity for VEGF are identified by
CC immunoprecipitation or by an in vitro binding assay
XX Sequence 118 AA;

Query Match 100.0%; Score 658; DB 3; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.6e-56;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGSGLRSLRSCAAGYDFTHYGMWVROAPGKLEWVGWINTYTGEPT 60
DB 1 EVOLVESGGGLVOPGSGLRSLRSCAAGYDFTHYGMWVROAPGKLEWVGWINTYTGEPT 60
61 AADPKRRFTPSLDTSKSTAYLQWNSLRADTAIVYCAKPYVYGTSHWYFDWVGQGL 118
61 AADPKRRFTPSLDTSKSTAYLQWNSLRADTAIVYCAKPYVYGTSHWYFDWVGQGL 118

RESULT 4
AAB13384
ID AAB13384 standard; protein; 118 AA.

AC AAB13384;
XX
DT 21-NOV-2000 (first entry)

XX Anti-VEGF antibody Y0313-1 heavy chain variable domain.

XX Y0313-1; vascular endothelial cell growth factor; VEGF; antibody;
KM antiinflammatory; cerebroprotective; cytoskeletal; antithumatic;
KM antiarthritic; antipsoriatic; antiarteriosclerotic; antidiabetic;
KM antithyroid; excessive neovascularisation; tumour; rheumatoid arthritis;
KM psoriasis; atherosclerosis; diabetes; retrolental fibroplasia;
KM neovascular glaucoma; haemangioma; thyroid hyperplasia; Grave's disease;
KM tissue transplantation; inflammation; oedema; trauma;
KM complementarity determining region; CDR.

XX Unidentified.

XX Key Location/Qualifiers
FH Region 26..35 /label= CDR-H1
FT Region 50..66 /label= CDR-H2
FT Region 70..79 /label= CDR-7
FT Region 99..112 /label= CDR-H3
FT Region 99..112 /label= CDR-H3

XX WO200037502-A2.

XX 29-JUN-2000.

XX 09-DEC-1999; 99WO-US029475.

XX 22-DEC-1998; 98US-00218481.

XX (GERTH) GENENTECH INC.

XX Van Bruggen N, Ferrara N;

XX WPI; 2000-442646/38.

XX Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis,
XX diabetes and chronic inflammation in a mammal, comprises administering a
XX human vascular endothelial cell growth factor antagonist.

XX Disclosure; Fig 14B; 60pp; English.

XX The present sequence is the heavy chain variable region of the affinity
XX matured anti-vascular endothelial cell growth factor (anti-VEGF) antibody

CC Y0313-1. Humanised F(ab)-12 and affinity matured anti-VEGF antibodies may
CC be used to treat conditions characterised by undesirable excessive
CC neovascularisation. Such conditions include tumours (especially solid
CC ones), rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and
CC other retinopathies, retrolental fibroplasia, age-related macular
CC degeneration, neovascular glaucoma, haemangiomas, thyroid hyperplasias
CC (including Grave's disease), corneal and other tissue transplantation,
CC and chronic inflammation. Oedemas associated with tumours, strokes and
CC head trauma, and ascites associated with malignancies, meigs' syndrome,
CC lung inflammation, nephrotic syndrome, pericardial effusion and pleural
CC effusion, may also be treated. Monoclonal antibodies are generated in
CC hybridoma cells and those with affinity for VEGF are identified by
CC immunoprecipitation or by an in vitro binding assay
XX Sequence 118 AA;

Query Match 100.0%; Score 658; DB 3; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.6e-56;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGSGLRSLRSCAAGYDFTHYGMWVROAPGKLEWVGWINTYTGEPT 60
DB 1 EVOLVESGGGLVOPGSGLRSLRSCAAGYDFTHYGMWVROAPGKLEWVGWINTYTGEPT 60
61 AADPKRRFTPSLDTSKSTAYLQWNSLRADTAIVYCAKPYVYGTSHWYFDWVGQGL 118
61 AADPKRRFTPSLDTSKSTAYLQWNSLRADTAIVYCAKPYVYGTSHWYFDWVGQGL 118

RESULT 5
ABP61255
ID ABP61255 standard; protein; 118 AA.

AC ABP61255;
XX
DT 20-SEP-2002 (first entry)

XX Humanised anti-VEGF Y0313-1 antibody variable heavy domain.

XX Cyostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
KM vascular endothelial growth factor; angiogenesis inhibitor; tumour;
KM retinal disorder; intracocular neovascular disorder; Y0313-1; heavy chain;
KM variable domain.

XX Homo sapiens.
OS Mus sp.
OS Synthetic.

XX Key Location/Qualifiers
FH Domain 26..35 /label= CDR-H1
FT Domain 50..66 /label= CDR-H2
FT Domain 70..79 /label= CDR-7
FT Domain 99..112 /label= CDR-H3
FT Domain 99..112 /label= CDR-H3

XX US2002032315-A1.

XX 14-MAR-2002.

XX 06-APR-1998; 98US-00056160.

XX 06-AUG-1997; 97US-0054856P.

XX (BACA/) BACA M.
XX (WELU/) WELLS U A.
XX (PREST/) PRESTA L G.
XX (LOWM/) LOWMAN H B.
XX (CHEN/) CHEN Y M.

XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX WPI, 2002-517920/55.
DR New humanised anti-VEGF (vascular endothelial growth factor) antibodies
XX or their variants, useful for inhibiting VEGF-induced angiogenesis in a
PT mammal, particularly for treating tumor or retinal disorders.
XX Example 3; Fig 10; 47pp; English.
XX The present invention relates to humanised anti-VEGF (vascular
CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
CC particularly those having a tumor or a retinal disorder e.g. intraocular
CC neovascular disorders. The present sequence is an exemplary heavy chain
CC variable domain of the humanised anti-VEGF antibody of the invention
SQ Sequence 118 AA;
Query Match 100.0%; Score 658; DB 5; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.6e-56;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EVQLVESGGGLVQPGGSLRLSCAASGYPFTHYGMNWVRQAPGKLEWGMINTTGEPT 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYPFTHYGMNWVRQAPGKLEWGMINTTGEPT 60
OY 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYYYGTSHWYFDVWGQGT 118
DB 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYYYGTSHWYFDVWGQGT 118
RESULT 6
ABP61257
ID ABP61257 standard; protein; 118 AA.
XX ABP61257;
AC 20-SEP-2002 (first entry)
XX
DT Humanised anti-VEGF Y0317 antibody variable heavy domain.
XX
DB Humanised anti-VEGF Y0317 antibody variable heavy domain.
XX
XX Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
KW retinal disorder; intraocular neovascular disorder; Y0317; heavy chain;
XX variable domain.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Domain 26..35
FT /label= CDR-H1
FT 50..66
FT /label= CDR-H2
FT 70..79
FT Domain /label= CDR-7
FT 99..112
FT /label= CDR-H3
XX
XX US2002032315-A1.
XX
XX 14-MAR-2002.
XX
XX 06-APR-1998; 98US-00056160.
XX
XX 06-AUG-1997; 97US-0054856P.
XX
XX (BACA/) BACA M.
XX (WELL/) WELLS J A.
XX (PRES/) PRESTA L G.
XX (LOWM/) LOWMAN H B.

PA (CHEN/) CHEN Y M.
XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
PI WPI, 2002-517920/55.
XX
DR WPI, 2002-517920/55.
XX
XX New humanized anti-VEGF (vascular endothelial growth factor) antibodies
PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
PT mammal, particularly for treating tumor or retinal disorders.
XX Claim 25; Fig 10; 47pp; English.
XX The present invention relates to humanised anti-VEGF (vascular
CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
CC particularly those having a tumor or a retinal disorder e.g. intraocular
CC neovascular disorders. The present sequence is an exemplary heavy chain
CC variable domain of the humanised anti-VEGF antibody of the invention
SQ Sequence 118 AA;
Query Match 100.0%; Score 658; DB 5; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.6e-56;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EVQLVESGGGLVQPGGSLRLSCAASGYPFTHYGMNWVRQAPGKLEWGMINTTGEPT 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYPFTHYGMNWVRQAPGKLEWGMINTTGEPT 60
OY 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYYYGTSHWYFDVWGQGT 118
DB 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKPYYYGTSHWYFDVWGQGT 118
RESULT 7
ADG31769
ID ADG31769 standard; protein; 123 AA.
XX ADG31769;
AC 26-FEB-2004 (first entry)
XX
DT V(H) domain of matured humanised murine anti-VEGF antibody SeqID3.
XX
DB V(H) domain of matured humanised murine anti-VEGF antibody SeqID3.
XX protein library; in silico; VEGF; vascular endothelial growth factor;
KW antibody; computational prediction; V(H) domain; mouse; murine.
XX
OS Synthetic.
OS Mus sp.
XX
XX WO2003099999-A2.
XX
XX 04-DEC-2003.
XX
XX 20-MAY-2003; 2003WO-US016037.
XX
XX 20-MAY-2002; 2002US-00153159.
XX
XX 20-MAY-2002; 2002US-00153176.
XX
XX (ABMA-) ABMAXIS INC.
XX
XX Luo P, Hsieh M, Zhong P, Wang C, Cao Y, Liu S;
PI WPI, 2004-035117/03.
XX
XX Constructing antibody libraries for generating protein libraries with
PT improved biological function comprising selecting from tester protein
PT sequences two peptide segments having 15 sequence identity with the lead
PT sequence.
XX
XX Disclosure; SEQ ID NO 3; 354pp; English.
XX

CC This invention relates to a novel method for the generation and screening
CC of a protein library in *silico*. Specifically, it refers to a high-
CC throughput method optimised for the identification of anti-VEGF (vascular
CC endothelial growth factor) antibodies with improved binding affinities
CC for their target antigen (VEGF), using computational prediction. The
CC present invention describes selecting proteins with a desirable function
CC based on their structural similarity to the target structural or
CC functional motif of a lead protein of interest. Accordingly, these
CC protein libraries are functionally biased with increased diversity so as
CC to increase the chance of identifying novel hits or combinations of
CC mutants with enhanced binding affinity. Furthermore, the sequence profile
CC based on the multiple structure alignment of the available lead structure
CC allows the sampling of a larger sequence space than by traditional,
CC multiple sequence alignment approaches. This polypeptide sequence is the
CC V(H) domain of affinity matured humanised murine anti-VEGF antibody, used
CC in an exemplification of the invention.

CC Sequence 123 AA;

Query Match 100.0%; Score 658; DB 8; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.7e-56;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWVROAPGKLEWGMINTYGEPT 60
1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWVROAPGKLEWGMINTYGEPT 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWVROAPGKLEWGMINTYGEPT 60
61 AADFKRRFTPSLDTSKSTAYVLQMNLSRAEDTAVYCAKPYPGYGTSHWYFDWGQSTL 118
61 AADFKRRFTPSLDTSKSTAYVLQMNLSRAEDTAVYCAKPYPGYGTSHWYFDWGQSTL 118
Db 61 AADFKRRFTPSLDTSKSTAYVLQMNLSRAEDTAVYCAKPYPGYGTSHWYFDWGQSTL 118

RESULT 8
ABP51953
ID ABP51953 standard; protein; 254 AA.

XX ABP51953;

DT 09-OCT-2002 (first entry)

XX Plasmid pY0317 anti-VEGF Fab amino acid sequence SEQ ID NO:2 #2.

XX Bacterial host: protease; degP; prc; sgr; anti-VEGF antibody; antibody;
XX huminised; Apoc2 ligand; anti-CD18; anti-tissue factor; 2C4; anti-CD20;
XX anti-vascular endothelial growth factor; anti-Her-2; anti-CD40; Fab;
XX anti-CD11a; Fab'; Fab'2; Fab'2-leucine zipper fusion; anti-VEGF Fab.

OS Mus sp.
OS Escherichia coli.
OS Synthetic.

XX Key Location/Qualifiers
XX Peptide 1..23
XX /label= signal

FT Protein 24..254
FT /label= anti-VEGF_Fab

XX WO200248376-A2.

XX 20-JUN-2002.

XX 07-DEC-2001; 2001WO-US047581.

XX 14-DEC-2000; 2000US-0256162P.

XX (GENTH) GENENTECH INC.

XX Chen CY;

XX WPI, 2002-583522/62.

XX N-PSDB; ABQ73919.

XX Novel Escherichia coli strain useful for producing polypeptide, deficient

PT in degP and prc encoding protease, and harboring mutant sgr gene, product
PT of gene suppresses growth phenotypes of strains harboring prc mutants.

XX Example 1; Fig 1D-E; 63pp; English.

XX The present invention describes an Escherichia coli strain (1) deficient
XX in chromosomal degP and prc gene, the product of mutant sgr gene
XX and harbouring a mutant sgr gene, the product of mutant sgr gene
XX suppresses growth phenotypes exhibited by strains harbouring prc mutants.
XX (1) is useful for producing a polypeptide, by culturing (1) comprising
XX nucleic acid encoding the polypeptide, which is heterologous to the
XX strain, such that the nucleic acid is expressed, and recovering the
XX heterologous polypeptide from the strain. The heterologous polypeptide is
XX proteolytically sensitive. Culturing of (1) is performed in a fermentor
XX under conditions of high- or low-cell density fermentation. The
XX polypeptide is recovered from the periplasm or culture medium of the
XX strain. The polypeptide is an antibody (humanised or full-length
XX antibody) or Apoc2 ligand. The antibody is an anti-CD18, anti-vascular
XX endothelial growth factor (VEGF), anti-tissue factor, 2C4, anti-Her-2,
XX anti-CD20, anti-CD40, or anti-CD11a antibody. The antibody is also an
XX antibody fragment having a light chain (kappa light chain). The antibody
XX fragment is a Fab, Fab', Fab'2 or Fab'2-leucine zipper fusion, anti-CD18
XX Fab'2-leucine zipper fusion, anti-tissue factor Fab'2-leucine zipper
XX fusion or anti-VEGF Fab, with or without a histidine or lysine tag, anti-
XX tissue factor Fab'2-leucine zipper fusion with a 6-histidine tag, or anti-
XX CD18 Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-CD18
XX Fab'2-leucine zipper fusion with a 6-lysine tag. The present sequence
XX represents an anti-VEGF Fab amino acid sequence from the present
XX invention

SO Sequence 254 AA;

Query Match 100.0%; Score 658; DB 5; Length 254;
Best Local Similarity 100.0%; Pred. No. 6.1e-56;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWVROAPGKLEWGMINTYGEPT 60
24 EVQLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWVROAPGKLEWGMINTYGEPT 83
Db 24 EVQLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWVROAPGKLEWGMINTYGEPT 83

Qy 61 AADFKRRFTPSLDTSKSTAYVLQMNLSRAEDTAVYCAKPYPGYGTSHWYFDWGQSTL 118
61 AADFKRRFTPSLDTSKSTAYVLQMNLSRAEDTAVYCAKPYPGYGTSHWYFDWGQSTL 141
Db 61 AADFKRRFTPSLDTSKSTAYVLQMNLSRAEDTAVYCAKPYPGYGTSHWYFDWGQSTL 141

RESULT 9
ABB81110
ID ABB81110 standard; protein; 476 AA.

XX ABB81110;

DT 05-NOV-2002 (first entry)

XX Anti-VEGF heavy chain fragment.

XX Immunoglobulin; promoter; cytosolic; antiinflammatory; immunomodulator;
XX neuroprotective; CD11; tissue factor; vascular endothelial growth factor;
XX VEGF.

XX Synthetic.

XX Key Location/Qualifiers

XX Peptide 1..23
XX /note= "STII signal sequence TIR-1"

FT Protein 24..476
FT /note= "anti-VEGF heavy chain"

XX WO200261090-A2.

XX 08-AUG-2002.

XX 13-DEC-2001; 2001WO-US048691.

PR 14-DEC-2000; 2000US-0256164P.
 XX (GENTH) GENENTECH INC.
 PA
 XX
 PI Simmons LC, Kilmowski L, Reilly DE, Yaneura DG;
 XX
 DR MPI: 2002-619253/66.
 XX N-PESDB; ABN86646.
 DR
 XX New polynucleotide comprising first and second promoter-cistron pairs,
 PT useful for diagnosing, treating or preventing diseases associated with
 PT abnormal expression and/or activity of antigens such as inflammatory
 PT disorders.
 PS
 XX Disclosure; Fig 21A-C; 104pp; English.
 XX
 CC The invention provides a polynucleotide, which encodes an immunoglobulin
 CC (Ig), comprising a first or second promoter-cistron pair consisting of a
 CC first or second promoter and cistron, respectively. The first cistron of
 CC the first promoter-cistron pair comprises a first translational
 CC initiation region (TIR-L) operably linked to a nucleic acid sequence
 CC encoding an Ig light chain and the second cistron of the second promoter-
 CC cistron pair comprises a second translational initiation region (TIR-H)
 CC operably linked to a nucleic acid sequence encoding an Ig heavy chain.
 CC Upon expression of the polynucleotide in a prokaryotic host cell, light
 CC and heavy chains are folded and assembled to form a biologically active
 CC Ig. The antibody of the invention is useful for diagnosing, treating or
 CC preventing diseases or conditions associated with abnormal expression and
 CC /or activity of one or more antigen molecules e.g. lymphoid malignancies,
 CC inflammatory, angiogenic, immunologic, neuronal, glial, astrocytic,
 CC hypothalamic or other glandular disorders. The present sequence
 CC represents the amino acid sequence of an anti-vascular endothelial growth
 CC factor (VEGF) heavy chain fragment of the cistron vector pXVG2AP11
 CC
 SQ Sequence 476 AA;
 XX
 XX
 Query Match 100.0%; Score 658; DB 5; Length 476;
 Best Local Similarity 100.0%; Pred. No. 1.2e-55;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVOLVESGGGLVOPGSLRLSCAASGYDFTHYGMNVRQAPKGLEWVGMINITYGEPT 60
 DB 24 EVQLVESGGGLVOPGSLRLSCAASGYDFTHYGMNVRQAPKGLEWVGMINITYGEPT 83
 QY 61 AADFKRRFTFSLDTSKSTAYLQMSLRADPTAVVYCAKPYPGYGTSHWYFDVWGQGL 118
 DB 84 AADFKRRFTFSLDTSKSTAYLQMSLRADPTAVVYCAKPYPGYGTSHWYFDVWGQGL 141
 RESULT 10
 ADO14129
 ID ADO14129 standard; protein; 476 AA.
 AC ADO14129;
 XX
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Plasmid pXVG2AP11 expression cassette heavy chain protein SEQ ID NO:9.
 XX
 XX antibody; variant heavy chain hinge region; immunoconjugate; cytostatic;
 KW immunosuppressive; immunotherapy; tumour; cancer; immune disorder;
 KW expression cassette; plasmid pXVG2AP11; anti-VEGF heavy chain.
 OS Synthetic.
 XX
 XX WO2004042017-A2.
 PN
 XX 21-MAY-2004.
 PD
 XX 30-OCT-2003; 2003WO-US034610.
 PF
 XX 31-OCT-2002; 2002US-0422952P.
 PR
 XX

PA (GENTH) GENENTECH INC.
 XX
 XX Reilly D, Yaneura DG;
 PI
 XX
 DR MPI: 2004-390607/36.
 XX N-PESDB; ADO14127.
 DR
 XX New antibody comprising a variant heavy chain hinge region incapable of
 PT inter-heavy chain disulfide linkage, useful for treating, preventing,
 PT diagnosing, delaying or preventing a disease, e.g. tumor, cancer or
 PT immune disorder.
 PS
 XX Example 1; SEQ ID NO 9; 124pp; English.
 XX
 CC The present invention describes an antibody comprising a variant heavy
 CC chain hinge region incapable of inter-heavy chain disulfide linkage. Also
 CC described: (1) an antibody lacking inter-heavy chain disulfide linkage;
 CC (2) an immunoconjugate comprising the antibody conjugated with a
 CC heterologous moiety; (3) a composition comprising the antibody or
 CC immunoconjugate, and carrier; (4) an article of manufacture comprising
 CC the composition in a container; (5) a polynucleotide encoding the
 CC antibody or immunoconjugate, or a variant immunoglobulin heavy chain
 CC incapable of inter-heavy chain disulfide linkage; (6) a recombinant
 CC vector for expressing the antibody or immunoconjugate; (7) a host cell
 CC comprising the recombinant vector; (8) expressing in a host cell an
 CC antibody or interest in which at least one inter-heavy chain disulfide
 CC linkage is eliminated, and recovering the antibody from the host cell;
 CC (9) an aglycosylated antibody produced by the method; and (10) treating,
 CC preventing, diagnosing, delaying or preventing a disease in a subject.
 CC The antibody has cytostatic and immunosuppressive activities, and can be
 CC used in immunotherapy. The antibody, immunoconjugate and methods are
 CC useful for treating, preventing, diagnosing, delaying or preventing a
 CC disease, e.g. tumour, cancer or immune disorder. The present sequence
 CC represents the anti-VEGF heavy chain from the expression cassette of
 CC plasmid pXVG2AP11, which is used in the exemplification of the present
 CC invention.
 SQ Sequence 476 AA;
 XX
 XX
 Query Match 100.0%; Score 658; DB 8; Length 476;
 Best Local Similarity 100.0%; Pred. No. 1.2e-55;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVOLVESGGGLVOPGSLRLSCAASGYDFTHYGMNVRQAPKGLEWVGMINITYGEPT 60
 DB 24 EVQLVESGGGLVOPGSLRLSCAASGYDFTHYGMNVRQAPKGLEWVGMINITYGEPT 83
 QY 61 AADFKRRFTFSLDTSKSTAYLQMSLRADPTAVVYCAKPYPGYGTSHWYFDVWGQGL 118
 DB 84 AADFKRRFTFSLDTSKSTAYLQMSLRADPTAVVYCAKPYPGYGTSHWYFDVWGQGL 141
 RESULT 11
 ADO90730
 ID ADO90730 standard; protein; 476 AA.
 AC ADO90730;
 XX
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Anti-VEGF antibody Y0317 heavy chain protein SEQ ID NO:7.
 XX
 XX antibody; antigen binding fragment; cell culture; variable domain;
 KW modified framework region; hypervariable region; cytostatic;
 KW antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
 KW tumour; inflammatory disorder; angiogenic disorder;
 KW immunological disorder; anti-VEGF antibody;
 KW anti vascular endothelial cell growth factor antibody; heavy chain.
 OS Homo sapiens.
 XX
 XX Synthetic.
 PN WO2004065417-A2.

XX 05-AUG-2004.
 PD 23-JAN-2004; 2004MO-US001844.
 PF 23-JAN-2003; 2003US-0442484P.
 PR (GERTH) GENENTECH INC.
 PA
 XX
 PI
 DR WPI: 2004-562149/54.
 DR N-PSDB; ADQ90702.
 XX
 PT Producing an antibody or antigen binding fragment in high yield in a cell
 PT culture, comprises expressing a variable domain with a modified framework
 PT region in a host cell.
 XX
 PS Example 2; SEQ ID NO 7; 161pp; English.
 CC The present invention describes a method for producing an antibody or
 CC antigen binding fragment in high yield in a cell culture. The method
 CC comprises expressing a variable domain of the antibody or antigen binding
 CC fragment comprising a modified framework region (FR) in a host cell, and
 CC recovering the antibody or antigen binding fragment variable domain
 CC comprising the modified framework from the host cell. The modified FR in
 CC the method described above has a substitution of at least one amino acid
 CC position with a different amino acid, where the different amino acid is
 CC the amino acid found at the corresponding FR position of a human subgroup
 CC variable domain consensus sequence that has a hypervariable region 1
 CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
 CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
 CC The antibody or antigen binding fragment variable domain comprises the
 CC modified FR that has improved yield in cell culture compared to an
 CC unmodified antibody or antigen-binding fragment. The antibody and antigen
 CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and
 CC immunomodulatory activities, and can be used in antibody therapy. The
 CC methods and compositions of the present invention are useful for
 CC producing antibodies or antigen binding fragments in cell culture, in
 CC particular for improving the yield of recombinant antibodies or antigen
 CC binding fragments in cell culture. The antibodies of the invention can be
 CC used to diagnose, treat, inhibit or prevent e.g. tumours and
 CC inflammatory, angiogenic and immunological disorders. The present
 CC sequence represents the heavy chain of an anti-VEGF (vascular endothelial
 CC cell growth factor) antibody, which is used in the exemplification of the
 CC present invention.
 CC
 XX Sequence 476 AA;
 SO
 Query Match 100.0%; Score 658; DB 8; Length 476;
 Best Local Similarity 100.0%; Pred. No. 1.2e-55;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVQLVSGGGLVOPGSGLRSLSCAASGYDFTYGMNVRQAPGKGLFVWGINTYGEPT 60
 DB 24 EVQLVSGGGLVOPGSGLRSLSCAASGYDFTYGMNVRQAPGKGLFVWGINTYGEPT 83
 QY 61 AADFKRRFTFSLDTSKSTAYLQWNSLRADTAAYVYCAKPYRYGTSWYFDVWGQGT 118
 DB 84 AADFKRRFTFSLDTSKSTAYLQWNSLRADTAAYVYCAKPYRYGTSWYFDVWGQGT 141
 RESULT 12
 ADF09953
 ID ADF09953 standard; protein; 117 AA.
 XX
 AC ADF09953;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Antibody heavy chain variable region 1C28 (7-4-1).
 XX
 KM Antibody; stability; solubility; antigen binding affinity;

KM variable region; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003074679-A2.
 XX
 PD 12-SEP-2003.
 XX
 PF 03-MAR-2003; 2003MO-US006598.
 XX
 PR 01-MAR-2002; 2002US-0360843P.
 PR 29-MAY-2002; 2002US-0384197P.
 XX
 PA (XENC-) XENCOR.
 XX
 PI Lazar GA, Desjarlais JR, Marshall SA, Dahlyat B;
 DR WPI: 2003-722066/58.
 XX
 PT Computer optimization of physicochemical properties of antibodies
 PT comprises analyzing the interactions of amino acids at variable
 PT positions.
 PS Disclosure; Fig 2a; 135pp; English.
 CC The present invention relates to a method for optimizing at least one
 CC physico-chemical property of an antibody by a computational screening
 CC method. The method comprises: receiving a template antibody structure;
 CC selecting at least one variable position belonging to the antibody
 CC structure; selecting at least one amino acid to be considered at the
 CC variable position(s); analyzing the interaction of each selected amino
 CC acid at each variable position with at least part of the remainder of the
 CC antibody, including the selected amino acids at other variable positions;
 CC and identifying a set of at least one antibody sequence with at least one
 CC optimized physico-chemical property. The method is useful for optimizing
 CC the physico-chemical properties of an antibody, especially the stability,
 CC solubility, or antigen binding affinity. The optimized antibody may be
 CC useful for treating a patient. The present sequence is an antibody
 CC variable region sequence used to illustrate the invention.
 CC
 XX Sequence 117 AA;
 SO
 Query Match 99.4%; Score 654; DB 7; Length 117;
 Best Local Similarity 100.0%; Pred. No. 6.3e-56;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVQLVSGGGLVOPGSGLRSLSCAASGYDFTYGMNVRQAPGKGLFVWGINTYGEPT 60
 DB 1 EVQLVSGGGLVOPGSGLRSLSCAASGYDFTYGMNVRQAPGKGLFVWGINTYGEPT 60
 QY 61 AADFKRRFTFSLDTSKSTAYLQWNSLRADTAAYVYCAKPYRYGTSWYFDVWGQGT 117
 DB 61 AADFKRRFTFSLDTSKSTAYLQWNSLRADTAAYVYCAKPYRYGTSWYFDVWGQGT 117
 RESULT 13
 ADF10058
 ID ADF10058 standard; protein; 117 AA.
 XX
 AC ADF10058;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE VEGF antibody heavy chain variable region 1C28.
 XX
 KM Antibody; stability; solubility; antigen binding affinity;
 KM variable region; human; VEGF.
 XX
 OS Homo sapiens.
 XX
 PN WO2003074679-A2.
 XX
 PD 12-SEP-2003.

XX 03-MAR-2003; 2003WO-US006598.
PF
XX
XX 01-MAR-2002; 2002US-0360843P.
PR
XX 29-MAY-2002; 2002US-0384197P.
PR
XX
PA (XENC-) XENCOR.
XX
PI Lazar GA, Desjarlais JR, Marshall SA, Dahiya B,
XX
XX WPI; 2003-722066/68.
XX
XX Computer optimization of physicochemical properties of antibodies
PT comprises analyzing the interactions of amino acids at variable
XX positions.
XX
XX Example 6; Fig 16a; 135pp; English.
XX
XX The present invention relates to a method for optimizing at least one
CC physico-chemical property of an antibody by a computational screening
CC method. The method comprises: receiving a template antibody structure;
CC selecting at least one variable position belonging to the antibody
CC structure; selecting at least one amino acid to be considered at the
CC variable position(s); analyzing the interaction of each selected amino
CC acid at each variable position with at least part of the remainder of the
CC antibody, including the selected amino acids at other variable positions;
CC and identifying a set of at least one antibody sequence with at least one
CC optimized physico-chemical property. The method is useful for optimizing
CC the physico-chemical properties of an antibody, especially the stability,
CC solubility, or antigen binding affinity. The optimized antibody may be
CC useful for treating a patient. The present sequence is an antibody
CC variable region sequence used to illustrate the invention.
XX
XX Sequence 117 AA;
SQ
Query Match 99.4%; Score 654; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.3e-56;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWVROAPGKLEWGMINTYTGEPY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWVROAPGKLEWGMINTYTGEPY 60
QY 61 AADPKRRFTPSLDTSKSTAYLQMNSLRAEDTAVVYCAKPYRYGTSNHYFPDWGGCT 117
DB 61 AADPKRRFTPSLDTSKSTAYLQMNSLRAEDTAVVYCAKPYRYGTSNHYFPDWGGCT 117
RESULT 14
AAW70682
ID AAW70682 standard; peptide; 118 AA.
XX
XX AAW70682;
AC
XX
XX 27-JAN-1999 (first entry)
DT
XX
XX Anti-VEGF humanised antibody variable heavy domain of variant Y0243-1.
DE
XX
XX Heavy variable domain; murine; humanised antibody;
KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
KW VEGF-induced angiogenesis; tumour; retinal disorder;
KW age-related macular degeneration; diabetic retinopathy;
KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
XX
XX Synthetic.
OS
XX Mue sp.
OS
XX Homo sapiens.
XX
XX WO9845331-A2.
PN
XX
XX 15-OCT-1998.
PD
XX
XX 03-APR-1998; 98WO-US006604.
PF

XX 07-APR-1997; 97US-00833504.
PR
XX 06-AUG-1997; 97US-00908469.
PR
XX
XX (GETH) GENENTECH INC.
XX
XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM,
XX
XX WPI; 1998-56837/48.
XX
XX New humanised antibody with affinity for vascular endothelial growth
PT factor - for treatment of tumours, retinal disease and other angiogenic
PT states, also related nucleic acid, vectors and transformed cells.
XX
XX Example 3; Fig 10B; 100pp; English.
XX
XX The present sequence represents a variable heavy domain of an affinity-
CC matured anti-vascular endothelial growth factor (anti-VEGF) antibody
CC variant. The sequence is used in the course of the invention to produce
CC the humanised anti-VEGF antibody of the invention. The humanised
CC antibodies are used to inhibit VEGF-induced angiogenesis, particularly
CC for treating or preventing tumours (of any type) and retinal disorders.
CC (e.g. age-related macular degeneration or diabetic retinopathy). They can
CC also be used to treat other conditions that involve angiogenesis, e.g.
CC rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc
XX
XX Sequence 118 AA;
SQ
Query Match 98.6%; Score 649; DB 2; Length 118;
Best Local Similarity 98.3%; Pred. No. 2e-55;
Matches 116; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWVROAPGKLEWGMINTYTGEPY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTYGMNWVROAPGKLEWGMINTYTGEPY 60
QY 61 AADPKRRFTPSLDTSKSTAYLQMNSLRAEDTAVVYCAKPYRYGTSNHYFPDWGGCT 118
DB 61 AADPKRRFTPSLDTSKSTAYLQMNSLRAEDTAVVYCAKPYRYGTSNHYFPDWGGCT 118
RESULT 15
AAB05900
ID AAB05900 standard; peptide; 118 AA.
XX
XX AAB05900;
AC
XX
XX 17-OCT-2000 (first entry)
DT
XX
XX F(ab)-12 antibody variant Y0238-3 heavy chain variable domain.
DE
XX
XX Humanised, F(ab)-12, heavy chain variable domain; antibody variant;
KW phage display; randomised library; cytotoxic; antiarteriosclerotic;
KW antiproliferative; antidiabetic; antiinflammatory; antiarteriosclerotic;
KW vascular endothelial growth factor; VEGF; breast cancer; lung cancer;
KW retinoblastoma; rheumatoid arthritis; psoriasis; atherosclerosis;
KW diabetic retinopathy; complementarity determining region; CDR.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX WO200029584-A1.
PN
XX
XX 25-MAY-2000.
PD
XX
XX 16-NOV-1999; 99WO-US027153.
PF
XX
XX 18-NOV-1998; 98US-0108945P.
PR
XX
XX (GETH) GENENTECH INC.
XX
XX Chen YM, Lowman HB, Muller Y;
XX

DR MPI: 2000-387797/33.

XX Antibody variants with higher binding affinity than native antibodies
PT useful for diagnosis, prevention and treatment of neoplastic and non-
PT neoplastic diseases comprises amino acid insertion in hypervariable
PT region.

XX Disclousure: Fig 1B; 110pp; English.

XX The present sequence is the heavy chain variable domain of the F(ab)-12
CC antibody variant Y0238-3. F(ab)-12 is a humanised anti-vascular
CC endothelial growth factor (VEGF) antibody. F(ab)-12 was the parent
CC antibody used in the production of a large number of antibody variants
CC containing randomised peptide inserts within the complementarity
CC determining regions (CDRs). Phage display libraries were subjected to
CC eight rounds of selection to isolate variants with an antigen binding
CC affinity at least two-fold stronger than the binding affinity of parent
CC antibody for the target VEGF antibody. The anti-VEGF antibody variants
CC may be useful in diagnostic assays for detecting expression of VEGF in
CC cells, tissue or serum. They may also be used in the prevention and
CC treatment of neoplastic diseases such as breast cancer, lung cancer and
CC retinoblastoma, and non-neoplastic diseases including rheumatoid
CC arthritis, psoriasis, atherosclerosis, and diabetic and other
CC proliferative retinopathies

XX Sequence 118 AA:

Query Match 98.6%; Score 649; DB 3; Length 118;

Best Local Similarity 98.3%; Pred. No. 2e-55; Mismatches 0; Indels 0; Gaps 0;

Matches 116; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 EVQLVESGGGLVQPGGSLRLGCAAGYDPETHYGMNWRQAPGKLEWYGMINTYGEPTY 60
   |||||
DB 1 EVQLVESGGGLVQPGGSLRLSCAAGYDPETHYGMNWRQAPGKLEWYGMINTYGEPTY 60
   |||||

QY 61 AADFKRRFTFSLDTSKSTAYLQMSLRADTAIVYCAKYPYYGTSHWYFDVMGGTL 118
   |||||
DB 61 AADFKRRFTFSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVMGGTL 118
   |||||
```

Search completed: March 14, 2005, 20:39:17
Job time : 95.4518 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2005, 20:30:13 ; Search time 24.3246 Seconds
(without alignments)
362.127 Million cell updates/sec

Title: US-09-723-752B-116

Perfect score: 658
Sequence: 1 EVOLVESGGGIVOPGSGRLR.....YPRYGTSHWTFDVGQCTL 118

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	649	98.6	118 4	US-09-440-781-97 Sequence 97, Appl
2	635	96.5	118 4	US-09-440-781-96 Sequence 96, Appl
3	627.5	95.4	121 4	US-09-440-781-99 Sequence 99, Appl
4	613.5	93.2	121 4	US-09-440-781-98 Sequence 98, Appl
5	611	92.9	491 4	US-10-011-125A-2 Sequence 2, Appl1
6	507.5	77.1	118 1	US-08-425-336-126 Sequence 126, App
7	507.5	77.1	118 1	US-08-488-113B-126 Sequence 126, App
8	507.5	77.1	118 1	US-08-477-484B-126 Sequence 126, App
9	507.5	77.1	118 2	US-08-646-360-126 Sequence 126, App
10	507.5	77.1	118 3	US-08-839-765-126 Sequence 126, App
11	507.5	77.1	118 3	US-09-136-389-126 Sequence 126, App
12	507.5	77.1	118 3	US-09-610-838-126 Sequence 126, App
13	507.5	77.1	118 3	US-09-711-485-126 Sequence 126, App
14	507.5	77.1	240 1	US-08-488-113B-147 Sequence 147, App
15	507.5	77.1	240 1	US-08-488-113B-148 Sequence 148, App
16	507.5	77.1	240 1	US-08-477-484B-147 Sequence 147, App
17	507.5	77.1	240 1	US-08-477-484B-148 Sequence 148, App
18	507.5	77.1	240 2	US-08-646-360-147 Sequence 147, App
19	507.5	77.1	240 2	US-08-646-360-148 Sequence 148, App
20	507.5	77.1	240 3	US-08-839-765-147 Sequence 147, App
21	507.5	77.1	240 3	US-08-839-765-148 Sequence 148, App
22	507.5	77.1	240 3	US-09-136-389-147 Sequence 147, App
23	507.5	77.1	240 3	US-09-136-389-148 Sequence 148, App
24	507.5	77.1	240 3	US-09-610-838-147 Sequence 147, App
25	507.5	77.1	240 3	US-09-610-838-148 Sequence 148, App
26	507.5	77.1	240 4	US-09-711-485-147 Sequence 147, App
27	507.5	77.1	240 4	US-09-711-485-148 Sequence 148, App

28	493.5	75.0	118 1	US-08-107-669D-29 Sequence 29, Appl
29	493.5	75.0	118 1	US-08-472-788A-29 Sequence 29, Appl
30	493.5	75.0	118 2	US-08-477-531B-29 Sequence 29, Appl
31	493.5	75.0	118 2	US-08-062-842A-29 Sequence 29, Appl
32	493.5	74.8	118 1	US-08-107-669D-67 Sequence 67, Appl
33	493.5	74.8	118 1	US-08-472-788A-89 Sequence 89, Appl
34	493.5	74.8	118 2	US-08-477-531B-67 Sequence 67, Appl
35	493.5	74.8	118 2	US-08-062-842A-89 Sequence 89, Appl
36	493.5	74.7	122 2	US-07-934-373C-20 Sequence 20, Appl
37	491.5	74.7	122 3	US-08-437-642B-20 Sequence 20, Appl
38	491.5	74.7	122 4	US-08-146-206C-20 Sequence 20, Appl
39	491.5	74.7	122 4	US-09-705-686C-20 Sequence 20, Appl
40	491.5	74.7	122 4	US-09-705-392A-20 Sequence 20, Appl
41	491.5	74.7	122 4	US-09-705-392A-20 Sequence 20, Appl
42	491.5	74.7	122 5	PCT-US93-07832-20 Sequence 20, Appl
43	490.5	74.5	122 2	US-07-934-373C-45 Sequence 45, Appl
44	490.5	74.5	122 3	US-08-437-642B-45 Sequence 45, Appl
45	490.5	74.5	122 4	US-08-146-206C-26 Sequence 26, Appl

ALIGNMENTS

```
RESULT 1
US-09-440-781-97
Sequence 97, Application US/09440781
Patent No. 6632926
GENERAL INFORMATION:
APPLICANT: Yvonne Man-yeet Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P146981
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 97
LENGTH: 118
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-118
OTHER INFORMATION: humanized antibody heavy chain variable domain
US-09-440-781-97

Query Match 98.6%; Score 649; DB 4; Length 118;
Best Local Similarity 98.3%; Pred. No. 7.8e-59;
Matches 116; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGIVOPGSGRLRSCAAGYDFTYGNMWRQARQKGLIEWGINTYGEPTY 60
DB 1 EVOLVESGGGIVOPGSGRLRSCAAGYDFTYGNMWRQARQKGLIEWGINTYGEPTY 60
QY 61 AADKRRRTFSLDPSKSTAYVQNMNSLRADTAIVYCAKYPYRGTSHWTFDVGQCTL 118
DB 61 AADKRRRTFSLDPSKSTAYVQNMNSLRADTAIVYCAKYPYRGTSHWTFDVGQCTL 118

RESULT 2
US-09-440-781-96
Sequence 96, Application US/09440781
Patent No. 6632926
GENERAL INFORMATION:
APPLICANT: Yvonne Man-yeet Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P146981
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 96
LENGTH: 118
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
```

NAME/KEY: artificial
LOCATION: 1-118
OTHER INFORMATION: humanized antibody heavy chain variable domain
US-09-440-781-96

Query Match 96.5%; Score 635; DB 4; Length 118;
Best Local Similarity 96.6%; Pred. No. 2, 1e-57;
Matches 114; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTYGMNVRQAPGKGLRWGINTTYGEPY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYFTNYGMNVRQAPGKGLRWGINTTYGEPY 60
QY 61 AADFRRTFTSLDTSKSTAYLQNNSLRAEDTAVYCAKPYHYGSHWYFDWGQGT 118
DB 61 AADFRRTFTSLDTSKSTAYLQNNSLRAEDTAVYCAKPYHYGSHWYFDWGQGT 118

RESULT 3

US-09-440-781-99
Sequence 99, Application US/09440781
Patent No. 6632926

GENERAL INFORMATION:
APPLICANT: Yvonne Man-yea Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99

SEQ ID NO 99
LENGTH: 121
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-121
OTHER INFORMATION: humanized antibody heavy chain variable domain
US-09-440-781-99

Query Match 95.4%; Score 627.5; DB 4; Length 121;
Best Local Similarity 95.0%; Pred. No. 1, 3e-56;
Matches 115; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTYGMNVRQAPGKGLRWGINTTYGEPY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTYGMNVRQAPGKGLRWGINTTYGEPY 60
QY 61 AADFRRTFTSLDTSKSTAYLQNNSLRAEDTAVYCAKPYHYGSHWYFDWGQGT 117
DB 61 AADFRRTFTSLDTSKSTAYLQNNSLRAEDTAVYCAKPYHYGSHWYFDWGQGT 120

QY 118 L 118
DB 121 L 121

RESULT 4

US-09-440-781-98
Sequence 98, Application US/09440781
Patent No. 6632926

GENERAL INFORMATION:
APPLICANT: Yvonne Man-yea Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99

SEQ ID NO 98
LENGTH: 121
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial

LOCATION: 1-121
OTHER INFORMATION: humanized antibody heavy chain variable domain
US-09-440-781-98

Query Match 93.2%; Score 613.5; DB 4; Length 121;
Best Local Similarity 93.4%; Pred. No. 3, 4e-55;
Matches 113; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTYGMNVRQAPGKGLRWGINTTYGEPY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYFTNYGMNVRQAPGKGLRWGINTTYGEPY 60
QY 61 AADFRRTFTSLDTSKSTAYLQNNSLRAEDTAVYCAKPYHYGSHWYFDWGQGT 117
DB 61 AADFRRTFTSLDTSKSTAYLQNNSLRAEDTAVYCAKPYHYGSHWYFDWGQGT 120

QY 118 L 118
DB 121 L 121

RESULT 5

US-10-011-125A-2
Sequence 2, Application US/1001125A
Patent No. 6828121

GENERAL INFORMATION:
APPLICANT: Chen, Christina Yu-Ching
TITLE OF INVENTION: BACTERIAL HOST STRAINS
FILE REFERENCE: P1804R1
CURRENT APPLICATION NUMBER: US/10/011,125A
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 12

SEQ ID NO 2
LENGTH: 491
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sequence is synthesized.
US-10-011-125A-2

Query Match 92.9%; Score 611; DB 4; Length 491;
Best Local Similarity 91.5%; Pred. No. 3, 2e-54;
Matches 108; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTYGMNVRQAPGKGLRWGINTTYGEPY 60
DB 261 EVQLVESGGGLVQPGGSLRLSCAASGYFTNYGMNVRQAPGKGLRWGINTTYGEPY 320
QY 61 AADFRRTFTSLDTSKSTAYLQNNSLRAEDTAVYCAKPYHYGSHWYFDWGQGT 118
DB 321 AADFRRTFTSLDTSKSTAYLQNNSLRAEDTAVYCAKPYHYGSHWYFDWGQGT 378

RESULT 6

US-08-425-336-126
Sequence 126, Application US/08425336
Patent No. 5621083

GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA

ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 31394
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-425-336-126

Query Match 77.1%; Score 507.5; DB 1; Length 118;
Best Local Similarity 77.8%; Pred. No. 2,1e-44;
Matches 91; Conservative 12; Mismatches 9; Indels 5; Gaps 1;
QY 1 EVLVESGGGLVPGGSLRLSCAASGYDFTHYGMNVRQAPGKGLVWGMINITYGPTY 60
DB 1 EILVQSGGGLVPGGSLRLSCAASGYDFTHYGMNVRQAPGKGLVWGMINITYGPTY 60
QY 61 AADFKRFTFSLDTSKSTAYLQWNSLRADTAAYVYCAKPYVYGTSHWYFDWGQGT 117
DB 61 ADFSKRFTFSLDTSKSTAYLQWNSLRADTAAYVYCAKPYVYGTSHWYFDWGQGT 112

RESULT 7
US-08-488-113B-126
Sequence 126, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B

FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-113B-126

Query Match 77.1%; Score 507.5; DB 1; Length 118;
Best Local Similarity 77.8%; Pred. No. 2,1e-44;
Matches 91; Conservative 12; Mismatches 9; Indels 5; Gaps 1;
QY 1 EVLVESGGGLVPGGSLRLSCAASGYDFTHYGMNVRQAPGKGLVWGMINITYGPTY 60
DB 1 EILVQSGGGLVPGGSLRLSCAASGYDFTHYGMNVRQAPGKGLVWGMINITYGPTY 60
QY 61 AADFKRFTFSLDTSKSTAYLQWNSLRADTAAYVYCAKPYVYGTSHWYFDWGQGT 117
DB 61 ADFSKRFTFSLDTSKSTAYLQWNSLRADTAAYVYCAKPYVYGTSHWYFDWGQGT 112

RESULT 8
US-08-477-484B-126
Sequence 126, Application US/08477484B
Patent No. 5756699
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-484B-126

Query Match 77.1%; Score 507.5; DB 1; Length 118;
Best Local Similarity 77.8%; Pred. No. 2.1e-44;
Matches 91; Conservative 12; Mismatches 9; Indels 5; Gaps 1;

QY 1 EVLVSGGGGLVPGGSLRLSCAAGYDFTYGNMWRQAPGKLEWVGINTYTGSEPTY 60
DB 1 EIQLVSGGGGLVPGGSLRLSCAAGYDFTYGNMWRQAPGKLEWVGINTYTGSEPTY 60
QY 61 AADPKRFTSLDTSKSTAYLQNNSLRAEDTAVYYCAKYPYYGTSNHYPDVWGQGT 117
DB 61 AADPKRFTSLDTSKSTAYLQNNSLRAEDTAVYYCAKYPYYGTSNHYPDVWGQGT 112

RESULT 9
US-08-646-360-126
Sequence 126, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studulka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-360-126

Query Match 77.1%; Score 507.5; DB 2; Length 118;
Best Local Similarity 77.8%; Pred. No. 2.1e-44;
Matches 91; Conservative 12; Mismatches 9; Indels 5; Gaps 1;

QY 1 EVLVSGGGGLVPGGSLRLSCAAGYDFTYGNMWRQAPGKLEWVGINTYTGSEPTY 60
DB 1 EIQLVSGGGGLVPGGSLRLSCAAGYDFTYGNMWRQAPGKLEWVGINTYTGSEPTY 60
QY 61 AADPKRFTSLDTSKSTAYLQNNSLRAEDTAVYYCAKYPYYGTSNHYPDVWGQGT 117
DB 61 AADPKRFTSLDTSKSTAYLQNNSLRAEDTAVYYCAKYPYYGTSNHYPDVWGQGT 112

RESULT 10
US-08-839-765-126
Sequence 126, Application US/08839765
Patent No. 614631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studulka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-839-765-126

Query Match 77.1%; Score 507.5; DB 3; Length 118;
Best Local Similarity 77.8%; Pred. No. 2.1e-44;
Matches 91; Conservative 12; Mismatches 9; Indels 5; Gaps 1;

QY 1 EVOLVSGGGLVPGGSLRLSCAAGYDFTHYGMNVRQAPGKLEWVGINTYGEPT 60
DB 1 EIQLVSGGGLVPGGSLRLSCAAGYDFTHYGMNVRQAPGKLEWVGINTYGEPT 60
QY 61 AADPKRFTFTSLDTSKSTAYLQNNSLRAEDTAVYCAKYPYVYGTSHWYFDVWGQT 117
DB 61 AADPKRFTFTSLDTSKSTAYLQNNSLRAEDTAVYCAKYPYVYGTSHWYFDVWGQT 117

RESULT 11
US-09-136-389-126
Sequence 126, Application US/09136389
Patent No. 6146850
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studulka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360

FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-136-389-126

Query Match 77.1%; Score 507.5; DB 3; Length 118;
Best Local Similarity 77.8%; Pred. No. 2.1e-44;
Matches 91; Conservative 12; Mismatches 9; Indels 5; Gaps 1;

QY 1 EVOLVSGGGLVPGGSLRLSCAAGYDFTHYGMNVRQAPGKLEWVGINTYGEPT 60
DB 1 EIQLVSGGGLVPGGSLRLSCAAGYDFTHYGMNVRQAPGKLEWVGINTYGEPT 60
QY 61 AADPKRFTFTSLDTSKSTAYLQNNSLRAEDTAVYCAKYPYVYGTSHWYFDVWGQT 117
DB 61 AADPKRFTFTSLDTSKSTAYLQNNSLRAEDTAVYCAKYPYVYGTSHWYFDVWGQT 117

RESULT 12
US-09-610-838-126
Sequence 126, Application US/09610838
Patent No. 6376217
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studulka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-JUL-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/136,389
FILING DATE: 18-AUG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-610-838-126

Query Match 77.1%; Score 507.5; DB 3; Length 118;
Best Local Similarity 77.8%; Pred. No. 2.1e-44;
Matches 91; Conservative 12; Mismatches 9; Indels 5; Gaps 1;
QY 1 EVLVESGGGLVPGGSLRLSCAASGYDFTHYGMMWRQAPGKLEWGMINTTGERPT 60
DB 1 EIQLVGGGGLVVRGSGVRISCAASGYTFYNYGMMWRQAPGKLEWGMINTTGERPT 60
QY 61 AADFKRFTSLDPSKSTAYLQWNSLRAPDTAVYCAKPYPGYGTSHYFPDWGCGT 117
DB 61 ADFKGRFTSLDPSKSTAYLQWNSLRAPDTAVYCAKPYPGYGTSHYFPDWGCGT 112

RESULT 13
US-09-711-485-126
Sequence 126, Application US/09711485
Patent No. 6649742
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/711,485

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/839,765
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-711-485-126

Query Match 77.1%; Score 507.5; DB 4; Length 118;
Best Local Similarity 77.8%; Pred. No. 2.1e-44;
Matches 91; Conservative 12; Mismatches 9; Indels 5; Gaps 1;
QY 1 EVLVESGGGLVPGGSLRLSCAASGYDFTHYGMMWRQAPGKLEWGMINTTGERPT 60
DB 1 EIQLVGGGGLVVRGSGVRISCAASGYTFYNYGMMWRQAPGKLEWGMINTTGERPT 60
QY 61 AADFKRFTSLDPSKSTAYLQWNSLRAPDTAVYCAKPYPGYGTSHYFPDWGCGT 117
DB 61 ADFKGRFTSLDPSKSTAYLQWNSLRAPDTAVYCAKPYPGYGTSHYFPDWGCGT 112

RESULT 14
US-08-488-113B-147
Sequence 147, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995

```

1  APPLICATION NUMBER: US 08/425,336
2  FILING DATE: 18-APR-1995
3  PRIOR APPLICATION DATA:
4  APPLICATION NUMBER: US 08/064,691
5  FILING DATE: 12-MAY-1993
6  PRIOR APPLICATION DATA:
7  APPLICATION NUMBER: US 07/988,430
8  FILING DATE: 09-DEC-1992
9  PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: US 07/901,707
11 FILING DATE: 19-JUN-1992
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: US 07/787,567
14 FILING DATE: 04-NOV-1991
15 ATTORNEY/AGENT INFORMATION:
16 NAME: McNicholas, Janet M.
17 REGISTRATION NUMBER: 32,918
18 REFERENCE/DOCKET NUMBER: 11020US07/200-70.P3.C2A
19 TELECOMMUNICATION INFORMATION:
20 TELEPHONE: 312/707-8889
21 TELEFAX: 312/707-9155
22 TELEX: 650 388-1248
23 INFORMATION FOR SEQ ID NO: 148:
24 SEQUENCE CHARACTERISTICS:
25 LENGTH: 240 amino acids
26 TYPE: amino acid
27 TOPOLOGY: linear
28 MOLECULE TYPE: protein
29 US-08-488-113b-148

```

```
QY      77.1%; Score 507.5; DB 1; Length 240;  
Query Match Best Local Similarity 79.8%; Pred. No. 4.8e-44;  
Matches 92; Conservative 12; Mismatches 9; Indels 5; Gaps  
  
QY      1 ENVLVSGGGIIVOPGSLRSCAASGYDDTHGMMVMVRAPKGLGEWMTNTTYGEPY 66  
    |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db     1 EIDLVSOGGLVPAGSVIRISCAASYTTTNGMNMVRAPKGLGEMKMINTHTGPY 60  
    |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
  
QY      ADDFKRFPFSLDTSKSTAYLWMNSLRADTAIVYCAPPYYGTSHVFDMVGQT 117  
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db     61 AHSFKRPFTFLSDDSNNTAYLTQINSLRADIAIVFCSTRGY-----DWTFEDMGQT 112  
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
```

RESULT 15
 US-08-488-113B-148
 Sequence 148, Application US/08488113B
 Patent No. 5744580
 GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 APPLICANT: Carroll, Stephen F.
 APPLICANT: Studnicks, Gary M.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 NUMBER OF INVENTION: Proteins
 NUMBER OF SEQUENCES: 169
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/488,113B
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using ew model

Run on: March 14, 2005, 20:22:02 ; Search time 43.9912 Seconds
(without alignments)
884.760 Million cell updates/sec

Title: US-09-723-752b-116

Perfect score: 658
Sequence: 1 EVOLVESGGGLVQPGCSURL.....YPIYYGTSHWYDVMGQGL 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubppaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubppaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubppaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubppaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	658	100.0	118	9	US-09-056-160B-116
2	658	100.0	118	9	US-09-056-160B-118
3	658	100.0	118	14	US-10-234-671-114
4	658	100.0	118	14	US-10-234-671-116
5	658	100.0	123	13	US-10-153-159-3
6	658	100.0	123	13	US-10-153-159-3
7	658	100.0	123	15	US-10-443-134A-3
8	658	100.0	123	16	US-10-723-434-56
9	658	100.0	224	16	US-10-379-392-136
10	658	100.0	224	16	US-10-379-392-138
11	658	100.0	476	14	US-10-379-392-140
12	658	100.0	476	14	US-10-020-786-11
13	658	100.0	476	17	US-10-697-995-9

14	654	99.4	117	16	US-10-379-392-58
15	653	99.2	224	16	US-10-379-392-148
16	650	98.8	117	16	US-10-379-392-122
17	649	98.6	118	9	US-09-056-160B-112
18	649	98.6	118	14	US-10-234-671-110
19	649	98.6	118	15	US-10-624-153-97
20	648	98.5	224	16	US-10-379-392-156
21	645	98.0	117	16	US-10-379-392-124
22	645	98.0	231	15	US-10-364-953-9
23	644	97.9	123	16	US-10-723-434-103
24	641	97.4	117	16	US-10-379-392-130
25	640	97.3	118	9	US-09-056-160B-114
26	640	97.3	118	14	US-10-234-671-112
27	640	97.3	231	15	US-10-364-953-5
28	638	97.0	123	16	US-10-443-134A-128
29	638	97.0	123	16	US-10-723-434-105
30	635	96.5	118	9	US-09-056-160B-108
31	635	96.5	118	14	US-10-234-671-7
32	635	96.5	118	14	US-10-234-671-106
33	635	96.5	118	15	US-10-624-153-96
34	635	96.5	123	9	US-09-056-160B-7
35	635	96.5	123	13	US-10-153-159-1
36	635	96.5	123	13	US-10-153-159-14
37	635	96.5	123	14	US-10-153-176-1
38	635	96.5	123	14	US-10-153-176-14
39	635	96.5	123	15	US-10-443-134A-14
40	635	96.5	123	16	US-10-723-434-55
41	635	96.5	123	15	US-10-723-434-55
42	635	96.5	231	17	US-10-877-532-8
43	635	96.5	231	15	US-10-364-953-2
44	633	96.2	123	15	US-10-443-134A-126
45	633	96.2	123	16	US-10-723-434-104

ALIGNMENTS

Sequence 58, App1
Sequence 148, App
Sequence 122, App
Sequence 112, App
Sequence 110, App
Sequence 97, App1
Sequence 156, App
Sequence 124, App
Sequence 9, App1
Sequence 103, App
Sequence 130, App
Sequence 114, App
Sequence 112, App
Sequence 5, App1
Sequence 128, App
Sequence 108, App
Sequence 108, App
Sequence 7, App1
Sequence 106, App
Sequence 96, App1
Sequence 7, App1
Sequence 1, App1
Sequence 14, App1
Sequence 1, App1
Sequence 14, App1
Sequence 14, App1
Sequence 14, App1
Sequence 55, App1
Sequence 8, App1
Sequence 2, App1
Sequence 126, App
Sequence 104, App

RESULT 1
US-09-056-160B-116
Sequence 116, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Beca, Manuel
APPLICANT: Welle, Manuel
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-1608-116

Query Match 100.0%; Score 658; DB 9; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.3e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGGSLRLSCAASGYDFTHYGMNWRQAPGKLEWVGINTYTGSEPTY 60
DB 1 EVOLVESGGGLVOPGGSLRLSCAASGYDFTHYGMNWRQAPGKLEWVGINTYTGSEPTY 60
61 AADFKRRFTSLDTSKSTAYLQNSLRADTAAYYCAKPYYYGTSHWYFDVWGQGL 118
61 AADFKRRFTSLDTSKSTAYLQNSLRADTAAYYCAKPYYYGTSHWYFDVWGQGL 118

RESULT 2

US-09-056-1608-118
Sequence 118, Application US/090561608
Patent No. US20020032315A1

GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056.1608
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-1608-118

Query Match 100.0%; Score 658; DB 9; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.3e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGGSLRLSCAASGYDFTHYGMNWRQAPGKLEWVGINTYTGSEPTY 60
118

DB 1 EVOLVESGGGLVOPGGSLRLSCAASGYDFTHYGMNWRQAPGKLEWVGINTYTGSEPTY 60
QY 61 AADFKRRFTSLDTSKSTAYLQNSLRADTAAYYCAKPYYYGTSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQNSLRADTAAYYCAKPYYYGTSHWYFDVWGQGL 118

RESULT 3

US-10-234-671-114
Sequence 114, Application US/10234671
Publication No. US20030190317A1

GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-Apr-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-Apr-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-10-234-671-114

Query Match 100.0%; Score 658; DB 14; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.3e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGGSLRLSCAASGYDFTHYGMNWRQAPGKLEWVGINTYTGSEPTY 60
DB 1 EVOLVESGGGLVOPGGSLRLSCAASGYDFTHYGMNWRQAPGKLEWVGINTYTGSEPTY 60
61 AADFKRRFTSLDTSKSTAYLQNSLRADTAAYYCAKPYYYGTSHWYFDVWGQGL 118
61 AADFKRRFTSLDTSKSTAYLQNSLRADTAAYYCAKPYYYGTSHWYFDVWGQGL 118

RESULT 4
US-10-234-671-116
Sequence 116, Application US/10234671

Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpactin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-10-234-671-116
Query Match 100.0%; Score 658; DB 14; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.3e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVOLVESGGGLVPGGSLRLSQAAGYDFTHYGMNWRQAPGKGLRWGINTYTGEPY 60
DB 1 EVOLVESGGGLVPGGSLRLSQAAGYDFTHYGMNWRQAPGKGLRWGINTYTGEPY 60
QY 61 AADFKRRFTSLDTSKSTAYLQNNSLRAEDTAVYCAKPYYYGTSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQNNSLRAEDTAVYCAKPYYYGTSHWYFDVWGQGL 118
RESULT 5
US-10-153-159-3
Sequence 3, Application US/10153159
Publication No. US20020177170A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
Hsieh, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Caili
TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY LIB
FILE REFERENCE: 26050-704
CURRENT APPLICATION NUMBER: US/10/153,159

CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 125
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH of matured anti-VEGF antibody
US-10-153-159-3
Query Match 100.0%; Score 658; DB 13; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.4e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVOLVESGGGLVPGGSLRLSQAAGYDFTHYGMNWRQAPGKGLRWGINTYTGEPY 60
DB 1 EVOLVESGGGLVPGGSLRLSQAAGYDFTHYGMNWRQAPGKGLRWGINTYTGEPY 60
QY 61 AADFKRRFTSLDTSKSTAYLQNNSLRAEDTAVYCAKPYYYGTSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQNNSLRAEDTAVYCAKPYYYGTSHWYFDVWGQGL 118
RESULT 7
US-10-443-134A-3
Sequence 3, Application US/10153176
Publication No. US20030022240A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
Hsieh, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Caili
APPLICANT: Cao, Yicheng
APPLICANT: Li, Shengjiang
APPLICANT: Liu, Shengjiang
TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO
FILE REFERENCE: 26050-701
CURRENT APPLICATION NUMBER: US/10/153,176
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 125
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH of matured anti-VEGF antibody
US-10-153-176-3
Query Match 100.0%; Score 658; DB 14; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.4e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVOLVESGGGLVPGGSLRLSQAAGYDFTHYGMNWRQAPGKGLRWGINTYTGEPY 60
DB 1 EVOLVESGGGLVPGGSLRLSQAAGYDFTHYGMNWRQAPGKGLRWGINTYTGEPY 60
QY 61 AADFKRRFTSLDTSKSTAYLQNNSLRAEDTAVYCAKPYYYGTSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQNNSLRAEDTAVYCAKPYYYGTSHWYFDVWGQGL 118

```
Sequence 3, Application US/10443134A
Publication No. US20040010376A1
GENERAL INFORMATION:
APPLICANT: Luo, Peizhi
APPLICANT: Hejeh, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Caoli
APPLICANT: Cao, Yicheng
APPLICANT: Liu, Shengjiang
TITLE OF INVENTION: GENERATION AND SELECTION OF PROTEIN LIBRARY IN SILICO
FILE REFERENCE: 26050-709
CURRENT APPLICATION NUMBER: US/10/443,134A
CURRENT FILING DATE: 2003-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: US 10/153,176
PRIOR FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/153,159
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH of matured anti-VEGF antibody
US-10-443-134A-3
```

```
Query Match      100.0%; Score 658; DB 15; Length 123;
Best Local Similarity 100.0%; Pred. No. 2,4e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 EVOLVESGGGLVOPGSLRLSCAASGYPFTHYGMMWRQAPGKGLEWVGMINITYGSEPT 60
D 1 EVOLVESGGGLVOPGSLRLSCAASGYDFTHYGNMWRQAPGKGLEWVGMINITYGSEPT 60
QY 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKYPYYGTSHWYFDWVGQGL 118
D 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKYPYYGTSHWYFDWVGQGL 118
```

```
RESULT 8
US-10-723-434-56
Sequence 56, Application US/10723434
Publication No. US20040133357A1
GENERAL INFORMATION:
APPLICANT: Zhong, Pingyu
APPLICANT: Luo, Peizhi
APPLICANT: Wang, Kevin C.
APPLICANT: Hejeh, Mark
APPLICANT: Li, Yan
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
FILE REFERENCE: 26050-709,501
CURRENT APPLICATION NUMBER: US/10/723,434
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 10/153,176
PRIOR FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/443,134
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PatentIn version 3.1
SEQ ID NO 56
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
```

```
OTHER INFORMATION: VH
US-10-723-434-56
```

```
Query Match      100.0%; Score 658; DB 16; Length 123;
Best Local Similarity 100.0%; Pred. No. 2,4e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 EVOLVESGGGLVOPGSLRLSCAASGYDFTHYGNMWRQAPGKGLEWVGMINITYGSEPT 60
D 1 EVOLVESGGGLVOPGSLRLSCAASGYDFTHYGNMWRQAPGKGLEWVGMINITYGSEPT 60
QY 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKYPYYGTSHWYFDWVGQGL 118
D 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKYPYYGTSHWYFDWVGQGL 118
```

RESULT 9

```
US-10-379-392-136
Sequence 136, Application US/10379392
Publication No. US20040110226A1
```

GENERAL INFORMATION:

APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjarlais, John Rudolf
APPLICANT: Marshall, Shannon Alicia

APPLICANT: Dahiyat, Basel I.

TITLE OF INVENTION: ANTIBODY OPTIMIZATION

FILE REFERENCE: A-71386-3 463077-236

CURRENT APPLICATION NUMBER: US/10/379,392

CURRENT FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: US 60/360,843

PRIOR FILING DATE: 2002-03-01

PRIOR APPLICATION NUMBER: US 60/384,197

PRIOR FILING DATE: 2002-05-29

NUMBER OF SEQ ID NOS: 184

SOFTWARE: PatentIn version 3.2

SEQ ID NO 136

LENGTH: 224

TYPE: PRT

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Humanized

```
Query Match      100.0%; Score 658; DB 16; Length 224;
Best Local Similarity 100.0%; Pred. No. 4,1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 EVOLVESGGGLVOPGSLRLSCAASGYDFTHYGNMWRQAPGKGLEWVGMINITYGSEPT 60
D 1 EVOLVESGGGLVOPGSLRLSCAASGYDFTHYGNMWRQAPGKGLEWVGMINITYGSEPT 60
QY 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKYPYYGTSHWYFDWVGQGL 118
D 61 AADFKRRFTSLDTSKSTAYLQWNSLRADTAIVYCAKYPYYGTSHWYFDWVGQGL 118
```

```
RESULT 10
US-10-379-392-138
Sequence 138, Application US/10379392
Publication No. US20040110226A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjarlais, John Rudolf
APPLICANT: Marshall, Shannon Alicia
APPLICANT: Dahiyat, Basel I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR FILING DATE: 2002-05-29
```


NUMBER OF SEQ ID NOS: 184
SOFTWARE: Patentin version 3.2
SEQ ID NO 138
LENGTH: 224
TYPE: PRT
ORGANISM: Artificial sequence
FEATURES:
OTHER INFORMATION: Synthetic
US-10-379-392-138

Query Match 100.0%; Score 658; DB 16; Length 224;
Best Local Similarity 100.0%; Pred. No. 4,1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGGSRLSCAASGYDFTHYGMNWRQAPGKLEWGMINTYTGEPY 60
DB 1 EVOLVESGGGLVOPGGSRLSCAASGYDFTHYGMNWRQAPGKLEWGMINTYTGEPY 60
DB 61 AADFKRRFTSLDTSKSTAYLQWNSLRABDTAVVYCAKPYPGTSHWYFDVWGQGL 118
61 AADFKRRFTSLDTSKSTAYLQWNSLRABDTAVVYCAKPYPGTSHWYFDVWGQGL 118

RESULT 11

US-10-379-392-140
Sequence 140, Application US/10379392
Publication No. US20040110226A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Marshall, John Rudolf
APPLICANT: Dahljat, Basel I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR FILING DATE: 2002-05-29
NUMBER OF SEQ ID NOS: 184
SOFTWARE: Patentin version 3.2
SEQ ID NO 140
LENGTH: 224
TYPE: PRT
ORGANISM: Artificial sequence
FEATURES:
OTHER INFORMATION: Synthetic
NAME/KEY: MISC FEATURE
LOCATION: (134)..(134)
OTHER INFORMATION: Xaa at position 134 can be Leu or Met
FEATURES:
NAME/KEY: MISC FEATURE
LOCATION: (189)..(189)
OTHER INFORMATION: Xaa at position 189 can be Val, Met, Ala or Ser
FEATURES:
NAME/KEY: MISC FEATURE
LOCATION: (191)..(191)
OTHER INFORMATION: Xaa at position 191 can be Val, Met or Ile
US-10-379-392-140

Query Match 100.0%; Score 658; DB 16; Length 224;
Best Local Similarity 100.0%; Pred. No. 4,1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGGSRLSCAASGYDFTHYGMNWRQAPGKLEWGMINTYTGEPY 60
DB 1 EVOLVESGGGLVOPGGSRLSCAASGYDFTHYGMNWRQAPGKLEWGMINTYTGEPY 60
QY 61 AADFKRRFTSLDTSKSTAYLQWNSLRABDTAVVYCAKPYPGTSHWYFDVWGQGL 118
61 AADFKRRFTSLDTSKSTAYLQWNSLRABDTAVVYCAKPYPGTSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQWNSLRABDTAVVYCAKPYPGTSHWYFDVWGQGL 118

RESULT 12
US-10-020-786-11
Sequence 11, Application US/10020786
Publication No. US20030073164A1
GENERAL INFORMATION:
APPLICANT: Simmons, Laura C.
APPLICANT: Klimowski, Laura
APPLICANT: Reilly, Dorothea
APPLICANT: Yansura, Daniel G.
TITLE OF INVENTION: PROKARYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF
FILE REFERENCE: PI793R1
CURRENT APPLICATION NUMBER: US/10/020,786
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/256,164
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 11
LENGTH: 476
TYPE: PRT
ORGANISM: Artificial sequence
FEATURES:
OTHER INFORMATION: anti-VEGF heavy chain
US-10-020-786-11

Query Match 100.0%; Score 658; DB 14; Length 476;
Best Local Similarity 100.0%; Pred. No. 8e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGGSRLSCAASGYDFTHYGMNWRQAPGKLEWGMINTYTGEPY 60
DB 24 EVOLVESGGGLVOPGGSRLSCAASGYDFTHYGMNWRQAPGKLEWGMINTYTGEPY 83
QY 61 AADFKRRFTSLDTSKSTAYLQWNSLRABDTAVVYCAKPYPGTSHWYFDVWGQGL 118
DB 84 AADFKRRFTSLDTSKSTAYLQWNSLRABDTAVVYCAKPYPGTSHWYFDVWGQGL 141

RESULT 13
US-10-697-995-9
Sequence 9, Application US/10697995
Publication No. US20050048572A1
GENERAL INFORMATION:
APPLICANT: Reilly, Dorothea
APPLICANT: Yansura, Daniel G.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INCREASING ANTIBODY PRODUCTION
FILE REFERENCE: 11669,195USU1
CURRENT APPLICATION NUMBER: US/10/697,995
CURRENT FILING DATE: 2003-10-30
PRIOR APPLICATION NUMBER: US 60/422,952
PRIOR FILING DATE: 2002-10-31
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 9
LENGTH: 476
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: anti-VEGF heavy chain
US-10-697-995-9

Query Match 100.0%; Score 658; DB 17; Length 476;
Best Local Similarity 100.0%; Pred. No. 8e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGGSRLSCAASGYDFTHYGMNWRQAPGKLEWGMINTYTGEPY 60
DB 24 EVOLVESGGGLVOPGGSRLSCAASGYDFTHYGMNWRQAPGKLEWGMINTYTGEPY 83
QY 61 AADFKRRFTSLDTSKSTAYLQWNSLRABDTAVVYCAKPYPGTSHWYFDVWGQGL 118
DB 84 AADFKRRFTSLDTSKSTAYLQWNSLRABDTAVVYCAKPYPGTSHWYFDVWGQGL 141

```

? TYPE/PRT      : Artificial sequence
? ORGANISM:
? FEATURE:
? OTHER INFORMATION: Synthetic
? FEATURE:
? NAME/KEY: MISC_FEATURE
? LOCATION: (5)..(5)
? OTHER INFORMATION: Xaa at position 5 can be Val or Arg
? FEATURE:
? NAME/KEY: MISC_FEATURE
? LOCATION: (132)..(132)
?

```

Search completed: March 14, 2005, 20:42:13
Job time : 44.9912 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: March 14, 2005, 20:39:29 ; Search time 17.8553 Seconds
(without alignments)
635,867 Million cell updates/sec

Title: US-09-723-752b-116

Perfect score: 658
Sequence: 1 EVQLVESGGGLVQPGGSLRL...YPRYGTSHWYFDWGQGL 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	427	64.9	138 2 S31666	Ig heavy chain V r
2	426	64.7	123 2 S31114	Ig heavy chain - h
3	426	64.7	131 2 S26792	Ig heavy chain V r
4	424	64.4	119 2 S31107	Ig heavy chain - h
5	418.5	63.6	120 2 B42848	Ig heavy chain V r
6	418.5	63.6	128 2 S48797	Ig heavy chain V r
7	418.5	63.6	146 4 S33905	Ig heavy chain pre
8	418	63.5	125 2 S30531	Ig heavy chain V r
9	416	63.2	123 2 S26794	Ig heavy chain V r
10	416	63.2	122 2 S19245	Ig heavy chain pre
11	415	63.1	127 2 S38489	Ig heavy chain - h
12	415	62.9	140 2 S31588	Ig heavy chain V r
13	414	62.9	140 2 S31686	Ig heavy chain V r
14	413.5	62.8	140 2 S70442	Ig heavy chain pre
15	412	62.6	119 2 A53285	Ig heavy chain V a
16	411.5	62.5	115 2 S19666	Ig heavy chain V r
17	411	62.5	121 2 S19666	Ig heavy chain V r
18	411	62.5	121 2 S31104	Ig heavy chain (au
19	411	62.5	160 2 S05271	Ig heavy chain pre
20	410.5	62.4	147 2 I37780	Ig variable region
21	409.5	62.2	119 2 S317453	Ig mu chain - huma
22	409	62.2	119 2 S31108	Ig heavy chain - h
23	408	62.0	119 2 D36005	Ig heavy chain V r
24	408	62.0	121 2 S15673	Ig heavy chain - h
25	407.5	61.9	114 2 D32667	Ig heavy chain V r
26	407	61.9	135 2 S31598	Ig heavy chain V r
27	407	61.9	143 2 S23624	Ig heavy chain V r
28	406.5	61.8	114 2 C32967	Ig heavy chain V r
29	406.5	61.8	124 2 S20782	Ig heavy chain V r

30	406	61.7	132 2 S31603	Ig heavy chain V r
31	405	61.6	120 1 M3HUBW	Ig heavy chain V-I
32	405	61.6	121 2 S31113	Ig heavy chain - h
33	402.5	61.2	120 2 S48798	Ig heavy chain V r
34	402	61.1	119 2 C36005	Ig heavy chain V r
35	401.5	61.0	124 1 AWM551	Ig heavy chain V r
36	401.5	61.0	128 1 S26786	Ig heavy chain V r
37	401.5	61.0	141 2 S31669	Ig heavy chain V r
38	401	60.9	117 2 S31109	Ig heavy chain V r
39	401	60.9	117 2 S36259	Ig heavy chain V r
40	400	60.8	123 1 AVMST5	Ig heavy chain V r
41	399.5	60.7	120 2 S25789	Ig heavy chain V r
42	399.5	60.7	122 2 S31117	Ig heavy chain - h
43	399	60.6	117 2 S32190	Ig heavy chain V r
44	399	60.6	123 2 PL0017	Ig heavy chain V-D
45	399	60.6	136 2 S35759	BHD9D10 protein -

ALIGNMENTS

RESULT 1

S31666 Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence _revision 10-Nov-1995 #text_change 23-Jul-1999

C/Accession: S31666

R/Submitter: A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31666

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-118 <CUI>

A/Cross-references: EMBL:244202; NID:g30963; PIDN:CAA78571.1; PID:g30964

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 64.9%; Score 427; DB 2; Length 138;
Best Local Similarity 70.3%; Pred. No. 1.3e-32;

Matches 83; Conservative 9; Mismatches 22; Indels 4; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYPSTHYQMNVRAQPGKLEWVGWINTYGEPTY 60

Db 20 EVQLVESGGGLVQPGGSLRLSCAASGFTSSVAMSVRAQPGKLEWVSAISGSGSTYY 79

Qy 61 AADFKRFTFTSDTSKSTAYLQNSLRADTAVYTCATKPYRYGTSHWYFDWGQGL 118

Db 80 ADSVKRFTISRDNKNTLYLQNSLRADTAVYCAK----ARTGYWFDLWGRGL 133

RESULT 2

S31114 Ig heavy chain - human

C/Species: Homo sapiens (man)

C/Date: 02-Dec-1993 #sequence _revision 26-May-1995 #text_change 17-Mar-1999

C/Accession: S31114

R/Submitter: P.M.; Timmerer, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmar

Bur, J. Immunol. 22, 247-251, 1992

A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complen

A/Reference number: S31104; M01D:92111633; PMID:1730252

A/Accession: S31114

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: mRNA

A/Residues: 1-123 <PDA>

A/Cross-references: EMBL:X62963

A/Note: The nucleotide sequence was submitted to the EMBL Data Library, October 1991

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

A:Submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from a
A:Reference number: S38488
A:Accession: S38489
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-127 <MAR>
A:Cross-references: EMBL:Z23028; NID:g414025; PIDN:CAA80563.1; PID:g414026
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98//Domain: immunoglobulin homology <IMM>

Query Match 63.1%; Score 415; DB 2; Length 127;
Best Local Similarity 66.1%; Pred. No. 1.6e-31;
Matches 82; Conservative 12; Mismatches 24; Indels 6; Gaps 2;

Oy 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTHTGMNWVRQAPKGLEWVGINTYGEPT 60
 :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1 QVLTVSGGGGVQPPGSLRLSCAASGFRTSSYAMSWVRQAPKGLEWVSALISGSGSTYY 60
 :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Oy 61 AADFKRRFTFLSDTSKSTAYLVQMNSLRADTAIVYCAK--YP---YYTGSHWYFDWG 114
 :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 61 ADSVGRFTISRDNKNTLYLQMSLRADTAIVYCAKEPFPADYDSGYSFYFDWG 120
 :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Oy 115 OGTL 118
 |||
Db 121 QGTLL 124
 |||

RESULT 12

S31586
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
A:Accession: S31588
R:Contributor: A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31588
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <CUI>
A:Cross-references: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-117//Domain: immunoglobulin homology <IMM>

Query Match 63.1%; Score 415; DB 2; Length 140;
Best Local Similarity 70.3%; Pred. No. 1.8e-31;
Matches 83; Conservative 9; Mismatches 24; Indels 2; Gaps 1;

Oy 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFTHTGMNWVRQAPKGLEWVGINTYGEPT 60
 |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 20 EQVLLESGGGLVQPGSLRLSCAASGFRTSSYAMSWVRQAPKGLEWVSALISGSGSTYY 79
 |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Oy 61 AADFKRRFTFLSDTSKSTAYLVQMNSLRADTAIVYCAKPYYYGTSHWYFDWGQCTL 118
 |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 80 ADSVGRFTISRDNKNTLYLQMSLRADTAIVYCAKHDI--SNVIYFDWGQCTL 135
 |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 13

S31686
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
A:Accession: S31686
R:Contributor: A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31685
A:Accession: S31686
A:Status: preliminary

A:Molecule type: mRNA
 A:Residues: 1-140 <CUI>
 A:Cross-references: EMBL:Z14205; NID:930969; PIDD:CAA76574.1; PID:g30970
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 62.9%; Score 414; DB 2; Length 140;
 Best Local Similarity 69.5%; Pred. No. 2,2e-31;
 Matches 82; Conservative 9; Mismatches 25; Indels 2; Gaps 1;

Oy 1 EVOLVESGGGVLPQGGSLRLSCAASGYDFTHTGMNMYRAQAPGKLEWYGMINTYTGEPY 60
 Db 20 EVQLLEGGGGLVQGGSLRLSCAASGFTFSYMSWRQAQPGKLEWVAISGSGSTYY 79
 Oy 61 AADFKRRPTSLDTSKSTAYLQNMNLSRAEDTAVYCAKPYRYGTSHTYFPDWGGTL 118
 Db 80 SDSYKGRFTISRDNKSTLYLQNMNLSRAEDTAVYCAKCPKPGSPS--FDYWGQTL 135

RESULT 14
 S70442
 Ig heavy chain precursor V region (mv) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
 C:Accession: S70442
 C:Cui: A.M.; Pimoux, F.; Fougereau, M.; Tonnelie, C.
 M.Ol. Immunol. 29, 1363-1373, 1992
 A:Title: Igm kappa/lambda Bv human B cell clone: an early step of differentiation of f
 A:Reference number: S70442; MUID:93024508; PMID:1383695
 A:Accession: S70442
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-140 <CUI>
 A:Cross-references: UNIPROT:Q8WUK1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 62.8%; Score 413.5; DB 2; Length 140;
 Best Local Similarity 70.6%; Pred. No. 2,4e-31;
 Matches 84; Conservative 11; Mismatches 19; Indels 5; Gaps 4;

Oy 1 EVOLVESGGGVLPQGGSLRLSCAASGYDFTHTGMNMYRAQAPGKLEWYGMINTYTGEPY 60
 Db 20 QVQLVESGGGVQPGSSRLSCAASGFTFSYGMHWQAQPGKLEWVAIFR-YGGSNKY 78
 Oy 61 AAD-FKRRPTSLDTSKSTAYLQNMNLSRAEDTAVYCAKPYRYGTSHTYFPDWGGTL 118
 Db 79 YADSVKGRFTISRDNKSTLYLQNMNLSRAEDTAVYCAK-RHIVGAT--YFPYWGQTL 134

RESULT 15
 A53285
 Ig heavy chain V and J regions, monoclonal antibody SCEN.M8.1 - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
 C:Accession: A53285
 R:Sanada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.
 Mol. Immunol. 28, 1063-1072, 1991
 A:Title: Molecular characterization of monoclonal anti-steroid antibodies: primary stru
 and their pH-reactivity profiles.
 A:Reference number: A53285; MUID:92017897; PMID:1922102
 A:Accession: A53285
 A:Status: preliminary
 A:Molecule type: DNA; protein
 A:Residues: 1-119 <SAM>
 A:Cross-references: GB:DJ2736; NID:g220595; PIDD:BA02228.1; PID:g220596
 A:Note: Sequence extracted from NCBI Backbone (NCBI:63271, NCBI:63289)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.6%; Score 412; DB 2; Length 119;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2005, 20:32:33 / Search time 82.807 Seconds

(without alignments)
729.713 Million cell updates/sec

Title: US-09-723-752B-116

Sequence: 1 EVOLVESGGGLVQPGGSLRL...YPPYGTSHWYFDVWGQCTL 118

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: uniprot_sprot:*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	414.5	63.0	475	2	Q6MZ06
2	414	62.9	597	2	Q6MBB9
3	413.5	62.8	241	2	Q921A6
4	406.5	61.8	118	2	Q9UL91
5	405	61.6	120	1	HV3E_HUMAN
6	404.5	61.5	122	1	HV21_MOUSE
7	402.5	61.2	605	2	Q6GMT2
8	401.5	61.0	573	2	Q8WUJ8
9	400	60.8	123	1	HV18_MOUSE
10	399	60.6	113	2	Q9UL90
11	398	60.5	123	1	HV19_MOUSE
12	398	60.5	472	2	Q6N0B9
13	396.5	60.3	473	2	Q6MZV7
14	395.5	60.1	112	2	Q9HCCI
15	395.5	60.1	613	2	Q6WUK1
16	394	59.9	478	2	Q6PI81
17	391	59.4	123	1	HV22_MOUSE
18	391	59.2	240	2	Q65ZC9
19	389.5	59.1	544	2	Q6RJ95
20	389	59.1	123	1	HV23_MOUSE
21	389	59.1	125	2	Q6PIL0
22	389	59.1	470	2	Q6PJU4
23	388.5	59.0	119	1	HV38_MOUSE
24	387	58.8	121	2	Q9UL71
25	386	58.7	464	2	Q6MZU6
26	384.5	58.4	122	1	HV20_MOUSE
27	384	58.4	487	2	Q80Z17
28	382	58.1	499	2	Q8NSK4
29	381	57.9	115	1	HV3D_HUMAN
30	381	57.9	123	1	HV24_MOUSE
31	379.5	57.7	119	1	HV37_MOUSE

32	379.5	57.7	147	2	Q9Y509	Q9Y509 homo sapien
33	379.5	57.7	487	2	Q6ZYX0	Q6ZYX0 homo sapien
34	378.5	57.5	493	2	Q6MZK9	Q6MZK9 homo sapien
35	378	57.4	493	2	Q6GMX2	Q6GMX2 homo sapien
36	375.5	57.1	122	1	HV3G_HUMAN	HV3G_HUMAN
37	375	57.0	123	1	HV25_MOUSE	HV25_MOUSE
38	374.5	56.9	119	1	HV40_MOUSE	HV40_MOUSE
39	374	56.8	484	2	Q9ULA6	Q9ULA6 mus musculus
40	374	56.8	485	2	Q6PDB8	Q6PDB8 mus musculus
41	372.5	56.6	116	2	Q683Y8	Q683Y8 mus musculus
42	372.5	56.6	118	2	Q9UL72	Q9UL72 homo sapien
43	372.5	56.6	122	2	Q9UL84	Q9UL84 homo sapien
44	372.5	56.6	136	1	HV16_MOUSE	HV16_MOUSE
45	371	56.4	470	2	Q7TWK1	Q7TWK1 mus musculus

ALIGNMENTS

RESULT 1	ID	Q6MZ06	PRELIMINARY;	PRT;	475 AA.
AC	Q6MZ06				
DT	05-JUL-2004	(TREMblrel. 27, Created)			
DT	05-JUL-2004	(TREMblrel. 27, Last sequence update)			
DT	05-JUL-2004	(TREMblrel. 27, Last annotation update)			
DE	Hypothetical protein DKFZp686G1190.				
GN	Name=DKFZp686G1190;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID:9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Human esophagus tumor;				
RG	The German Human cDNA Consortium;				
RA	Lauber J., Bahr A., Mewes H.W., Well B., Amid C., Osanger A., Fobo G.,				
RA	Han M., Wiemann S.,				
RL	Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BX640947; CAE45972.1; -				
DR	HSSP; P01861; IADQ.				
DR	InterPro; IPR003599; IG.				
DR	InterPro; IPR007110; IG-like.				
DR	InterPro; IPR003597; IG-cl.				
DR	InterPro; IPR003006; IG_MHC.				
DR	InterPro; IPR003596; IG_v.				
DR	PIfam; PF07654; C1-set; 3.				
DR	SMART; SM00409; IG; 2.				
DR	SMART; SM00407; IGcl; 3.				
DR	SMART; SM00406; IGV; 1.				
DR	PROSITE; PS50835; IG_LIKE; 4.				
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.				
KW	Hypothetical protein.				
SQ	SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;				
Query Match		63.0%;	Score 414.5;	DB 2;	Length 475;
Best Local Similarity		68.0%;	Pred. No. 7.7e-35;		
Matches	83;	Conservative 13;	Mismatches 21;	Indels 5;	Gaps 3;
QY	1	EVOLVESGGGLVQPGGSLRLCAASGYDFTHYGMNVRQAPGKGLBFWGMINITYGSPTY	60		
DB	20	EVOLVESGGGLVQPGGSLRLCAASGYDFTHYGMNVRQAPGKGLBFWGMINITYGSPTY	78		
QY	61	AAD-FKRRTFSDTSTKSTAYLQNSLRADTAVYYCAK--YPPYGTSHWYFDVWGQG	116		
DB	79	YADSVKGRFTISDSTNTLYLQNSLRADTAVYYCAKADYRDYQVSPAWYFDVWGGRG	138		
QY	117	TL 118			
DB	139	TL 140			
RESULT 2					

```
096BB9
ID 096BB9 PRELIMINARY; PRT; 597 AA.
AC 096BB9
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
[1]
SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helch F.,
RA Dlatcenko L., Marubia K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fehey J., Helton E., Kesteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywnicki M.I., Skalka U., Smalls D.E., Scherch A., Schin J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strauberg R.;
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015760; AAH15760.1; -.
DR PIR; S05271; S05271.
DR PIR; S24260; S24260.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65039 MW; 4FC3AD8EC263D9 CRC64;
```

```
01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Anti-CEA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819(1997).
DR EMBL; U88067; AAB48044.1; -.
DR PIR; S19965; S19965.
DR PIR; S19967; S19967.
DR PIR; S19968; S19968.
DR PIR; S26325; S26325.
DR HSSP; P01607; 1BWV.
DR SMART; SM00406; IGV_2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;
```

Query Match 62.8%; Score 413.5; DB 2; Length 241;
Best Local Similarity 64.1%; Pred. No. 4,7e-35;
Matches 75; Conservative 17; Mismatches 20; Indels 5; Gaps 1;

```
09
1 EVOLVESGGLVQPGSLRLSCAAGYDFTYHGMMVWQAPGKGLVWGINITYGSEPT 60
Db 1 QVRLQSGPELKKRGETVKISCAAGTPTDYGMMVWQAPGKGLVWGINITYGSEPT 60
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Qy 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
Db 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 117
61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKPYVYGTSHWYF--DVGQGT 1
```

Query Match 61.8%; Score 406.5; DB 2; Length 118;
 Best Local Similarity 67.8%; Pred. No. 1.2e-34;
 Matches 80; Conservative 11; Mismatches 22; Indels 5; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLSCAASGYDFTHYGMNWRQAPGKLEWVGNINTYGPPT 60
 |||||
 DB 1 EVOLVESGGGLVPGGSLRLSCAASGYDFTHYGMNWRQAPGKLEWVGNINTYGPPT 60
 |||||

QY 1 AADPKRFTSLDTSKSTAYLQNSLRADDTAVYYCAKYYVYGTSHWYDVGQGL 118
 |||||
 DB 61 AADPKRFTSLDTSKSTAYLQNSLRADDTAVYYCAKYYVYGTSHWYDVGQGL 118
 |||||

RESULT 5
 HV3E_HUMAN STANDARD; PRT; 120 AA.
 ID HV3E_HUMAN STANDARD; PRT; 120 AA.
 AC P01766;
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig heavy chain V-II region BRO.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=77117674; PubMed=65324; DOI=10.1016/0019-2791(76)90271-8;
 RX Capra J.D., Hopper J.E.;
 RT "Comparative studies on monocytic IgM lambda and IgG kappa from an
 RT individual patient. II. The complete amino acid sequence of the VH
 RT region of the IgM paraprotein."
 RL Immunochimistry 13:995-999(1976).
 CC -1- MISCELLANEOUS: This chain was obtained from IgM isolated from the
 CC serum of a patient with malignant lymphoma of the Waldenstrom
 CC type.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02049; M3HUBW.
 DR HSSP; P01783; 1IGC.
 DR GO; GO:000576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 111 Ig-like.
 FT NON_TER 120 120
 SQ SEQUENCE 120 AA; 13227 MW; D3F0428F7C2E6410 CRC64;

Query Match 61.8%; Score 405; DB 1; Length 120;
 Best Local Similarity 65.4%; Pred. No. 1.7e-34;
 Matches 83; Conservative 8; Mismatches 20; Indels 16; Gaps 3;

QY 1 EVOLVESGGGLVPGGSLRLSCAASGYDFTHYGMNWRQAPGKLEWVGNINTYGPPT 60
 |||||
 DB 1 EVOLVESGGGLVPGGSLRLSCAASGYDFTHYGMNWRQAPGKLEWVGNINTYGPPT 60
 |||||

QY 1 AADPKRFTSLDTSKSTAYLQNSLRADDTAVYYCAKYYVYGTSHWYDVGQGL 111
 |||||
 DB 60 AADPKRFTSLDTSKSTAYLQNSLRADDTAVYYCAKYYVYGTSHWYDVGQGL 111
 |||||

QY 112 VMGQGLT 118
 |||||
 DB 114 VMGQGLT 120
 |||||

RESULT 6
 HV21_MOUSE STANDARD; PRT; 122 AA.
 ID HV21_MOUSE STANDARD; PRT; 122 AA.

AC P01790;
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig heavy chain V region M511.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=81054880; PubMed=6776528;
 RX Robinson E.A., Appella E.;
 RT "Complete amino acid sequence of a mouse immunoglobulin alpha chain
 RT (MOPC 511)."
 RL Proc. Natl. Acad. Sci. U.S.A. 77:4909-4913(1980).
 CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that
 CC binds phosphorylcholine.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR HSSP; P01789; 1MCP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 114 Ig-like.
 FT NON_TER 122 122
 SQ SEQUENCE 122 AA; 13652 MW; 9F483731EA50207 CRC64;

Query Match 61.5%; Score 404.5; DB 1; Length 122;
 Best Local Similarity 65.3%; Pred. No. 1.9e-34;
 Matches 79; Conservative 13; Mismatches 20; Indels 9; Gaps 3;

QY 1 EVOLVESGGGLVPGGSLRLSCAASGYDFTHYGMNWRQAPGKLEWVGNINTYTG 56
 |||||
 DB 1 EVOLVESGGGLVPGGSLRLSCAASGYDFTHYGMNWRQAPGKLEWVGNINTYTG 60
 |||||

QY 57 EPTVADPKRFTSLDTSKSTAYLQNSLRADDTAVYYCAKYYVYGTSHWYDVGQGL 116
 |||||
 DB 61 E-YSASVGRFVSDTSKSTAYLQNSLRADDTAVYYCAKYYVYGTSHWYDVGQGL 115
 |||||

QY 117 T 117
 |||||
 DB 116 T 116
 |||||

RESULT 7
 O6GMV2 PRELIMINARY; PRT; 606 AA.
 ID O6GMV2 PRELIMINARY; PRT; 606 AA.
 AC O6GMV2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

```

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywni M.I., Skalka U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073758; AAH73758.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; Cl-sec; 4.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 606 AA; 66184 MW; BB838B5114E4C55 CRC64;

Query Match 61.2%; Score 402.5; DB 2; Length 606;
Best Local Similarity 59.4%; Pred. No. 1.8e-33;
Matches 79; Conservative 14; Mismatches 19; Indels 21; Gaps 2;

QY 1 EVLVESGGGLVPGGSLRLSCAASGYDFTHYGMNVRQAPGKLEWYGINITYGPTY 60
DB 20 QVLVESGGGLVPGGSLRLSCAASGYDFTSDYIMSWIQAPGKLEWYISSSSTINY 79
QY 61 AADFKRPTFSLTSTAYLQNMNLSRAEDTAVYYCAK-----PYYYG 104
DB 80 ADSVKGFTISRDNKNSLYLQNMNLSRAEDTAVYYCAAGNGIAAGRVAEDYVYYG 139
QY 105 TSHWYFDWGGGT 117
DB 140 -----MDVWGGGT 147

RESULT 8
ID Q8WU38 PRELIMINARY; PRT; 573 AA.
AC Q8WU38;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RL MEDLINE=238825; PubMed=2477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Datschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Umedin T.B., Toshimiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

```

```

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywni M.I., Skalka U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021276; AAH21276.1; -.
DR PIR; S21205; S21205.
DR PIR; S30532; S30532.
DR HSP; P18529; 118K.
DR Pfam; PF07654; Cl-sec; 2.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match 61.0%; Score 401.5; DB 2; Length 573;
Best Local Similarity 65.9%; Pred. No. 2.2e-33;
Matches 81; Conservative 9; Mismatches 22; Indels 11; Gaps 2;

QY 1 EVLVESGGGLVPGGSLRLSCAASGYDFTHYGMNVRQAPGKLEWYGINITYGPTY 60
DB 20 EVLVESGGGLVPGGSLRLSCAASGYDFTDYMHWVRQAPGKLEWYGISWNSGISY 79
QY 61 AADFKRPTFSLTSTAYLQNMNLSRAEDTAVYYCAK-----PYVGTSHWYFDW 114
DB 80 ADSVKGFTISRDNKNSLYLQNMNLSRAEDTAVYYCAKSGSGSYIGYYG----MDVW 134
QY 115 QGT 117
DB 135 QGT 137

RESULT 9
ID HV18 MOUSE STANDARD; PRT; 123 AA.
AC P01787;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V regions TEPC 15/S107/HPCM1/HPCM2/HPCM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (TEPC 15).
RX MEDLINE=6222762; PubMed=819932;
RA Rudikoff S., Potter M.;
RT "Size differences among immunoglobulin heavy chains from
RT phosphorylcholine-binding proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
RN [2]
RP SEQUENCE FROM N.A. (H107).
RX MEDLINE=8019926; PubMed=6769593; DOI=10.1016/0092-8674(80)90089-6;
RA Early P., Huang H., Davis M., Calame K., Hood L.;
RT "An immunoglobulin heavy chain variable region gene is generated from
RT three segments of DNA: VH, D and JH."
RL Cell 19:981-992(1980).
RN [3]
RP SEQUENCE (S107).

```

RX MEDLINE=76110488; PubMed=813561;
 RX DOI=10.1146/annurev.ge.09.120175.001513;
 RA Rudikoff S., Barstead P., Potter M., Hood L.;
 RL Unpublished results, cited by:
 RL Hood L., Campbell J.H., Elgin S.C.R.;
 RL Annu. Rev. Genet. 9:305-353(1975).
 [4]
 RP SEQUENCE (HPCW1; HPCW2 AND HPCW3).
 RX MEDLINE=81197602; PubMed=7231520;
 RA Geathart P.J., Johnson N.D., Douglas R., Hood L.;
 RT "IgG antibodies to phosphorylcholine exhibit more diversity than their
 RT IgM counterparts";
 RL Nature 291:29-34(1981).
 CC -1- MISCELLANEOUS: All those sequence appears to be identical,
 CC hydridoma proteins that bind phosphorylcholine.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A93804; AVMST5.
 DR HSSP; P01789; IMCP.
 DR InterPro; IPR007110; Ig_1like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SMO0406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Direct protein sequencing; Hybridoma; Immunoglobulin V region.
 FT DOMAIN 1 114
 FT NON_TER 123
 SQ SEQUENCE 123 AA; 13777 MW; 9D58086DE12F7000 CRC64;
 Query Match 60.8%; Score 400; DB 1; Length 123;
 Best Local Similarity 65.3%; Pred. No. 5,8e-34;
 Matches 79; Conservative 12; Mismatches 22; Indels 8; Gaps 3;
 QY 1 EVLVESGGGLVQPGGSLRLSCAAGYDFTYGMWVRQAPGKGLIEWV---GMINTYTG 56
 DB 1 EVLVESGGGLVQPGGSLRLSCATSGFTPSDFYMEWRQPGKRLIEWIAAARNKNDYTT 60
 QY 57 EPTVAADFKRRFTSLDTSKSTAYLQNMNLSLAEDTAVYYCAKPYRYGTSNHYFPVWGQG 116
 DB 61 E--YSASVKGRIIVSRDTSQSILYLQNMNLSLAEDTAVYYCAR--DYGSYWFYDVGAG 116
 QY 117 T 117
 DB 117 T 117
 RESULT 10
 Q9UL90 PRELIMINARY; PRT; 113 AA.
 AC Q9UL90;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614914; DOI=10.1006/clin.1998.4531;
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035024; AAD56260.1; -.
 DR PIR; S78486; S78486.
 DR HSSP; P01772; 2F84.
 DR InterPro; IPR007110; Ig_1like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SMO0406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 113
 SQ SEQUENCE 113 AA; 12437 MW; ED57EPDD19086D07F CRC64;
 Query Match 60.6%; Score 399; DB 2; Length 113;
 Best Local Similarity 69.7%; Pred. No. 6,7e-34;
 Matches 83; Conservative 6; Mismatches 18; Indels 12; Gaps 3;
 QY 1 EVLVESGGGLVQPGGSLRLSCAAGYDFTYGMWVRQAPGKGLIEWVGMINTYGEPT 60
 DB 1 EVLVESGGGLVQPGGSLRLSCAAGFTFSYGGMWVRQAPGKGLIEWAFIR-YDGSNXY 59
 QY 61 AAD-FKRRFTSLDTSKSTAYLQNMNLSLAEDTAVYYCAKPYRYGTSNHYFPVWGQTL 118
 DB 60 YADSVKGRFTISRDNSKNTLYLQNMNLSLAEDTAVYYCAKDLNY-----WQGGTL 108
 RESULT 11
 HV19 MOUSE
 ID HV19 MOUSE STANDARD; PRT; 123 AA.
 AC P01788;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig heavy chain V region H8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RA Barstead P.;
 RL Theis (1975), California Institute of Technology / Pasadena, U.S.A.
 CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that
 CC binds phosphorylcholine.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR HSSP; P01789; IMCP.
 DR InterPro; IPR007110; Ig_1like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; IGV; 1.
 DR SMART; SMO0406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 114
 FT NON_TER 123
 SQ SEQUENCE 123 AA; 13805 MW; 9D581401912F7000 CRC64;
 Query Match 60.5%; Score 398; DB 1; Length 123;
 Best Local Similarity 65.3%; Pred. No. 9,4e-34;
 Matches 79; Conservative 11; Mismatches 23; Indels 8; Gaps 3;
 QY 1 EVLVESGGGLVQPGGSLRLSCAAGYDFTYGMWVRQAPGKGLIEWV---GMINTYTG 56
 DB 1 EVLVESGGGLVQPGGSLRLSCATSGFTPSDFYMEWRQPGKRLIEWIAAARNKNDYTT 60
 QY 57 EPTVAADFKRRFTSLDTSKSTAYLQNMNLSLAEDTAVYYCAKPYRYGTSNHYFPVWGQG 116
 DB 61 E--YSASVKGRIIVSRDTSQSILYLQNMNLSLAEDTAVYYCAR--DYGSYWFYDVGAG 116
 QY 117 T 117
 DB 117 T 117
 RESULT 12
 G6N089 PRELIMINARY; PRT; 472 AA.
 ID G6N089
 AC G6N089;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686p15220.

GN Name=DKFZp686p15220;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human rectum tumor;
 RG The German Human CDNA Consortium;
 RA Wambut R., Heubner D., Mewes H.W., Weil B., Amid C., Oeanger A.,
 RA Pobo G., Han M., Wiemann S.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BX640827; CAB45781.1; -.
 DR HSP: P01861; IADO.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003597; IG_C1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF07654; C1-rec; 3.
 DR SMART: SM00409; IG; 2.
 DR SMART: SM00407; IG1; 3.
 DR PROSITE: PS50835; IG LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
 DR Hypothetical protein.
 KM SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;
 SQ

Query Match 60.5%; Score 398; DB 2; Length 472;
 Best Local Similarity 66.4%; Pred. No. 4,1e-33;
 Matches 81; Conservative 7; Mismatches 24; Indels 10; Gaps 2;

QY 1 EVQLVESGGGLVQPGSLRLSCAASGYDFTYGMNVRQAQPKGLEWGMINTYGEPT 60
 DB 20 EVQLVESGGGLVQPGSLRLSCAASGYDFTYGMNVRQAQPKGLEWGMINTYGEPT 79
 QY 61 AADPKRRFTSLDTSKSTAYLQNSLRADPTAVYCAKPY-----YYGTSNHYFPYWGQ 115
 DB 80 ADSVKGRTISRDNAKNSLYLQNSLRADPTAVYCAKPYGHNHYG----MDVWQD 134
 QY 116 GT 117
 DB 135 GT 136

RESULT 13
 QMZYV7
 ID 06MZV7; PRELIMINARY; PRT; 473 AA.
 AC 06MZV7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein DKFZp686C11235.
 GN Name=DKFZp686C11235;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human small intestine;
 RG The German Human CDNA Consortium;
 RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Oeanger A.,
 RA Pobo G., Han M., Wiemann S.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BX640853; CAB45920.1; -.
 DR HSP: P01861; IADO.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003597; IG_C1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF07654; C1-rec; 3.

DR SMART: SM00409; IG; 2.
 DR SMART: SM00407; IG1; 3.
 DR SMART: SM00406; IG1; 1.
 DR PROSITE: PS50835; IG LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
 DR Hypothetical protein.
 KM SEQUENCE 473 AA; 52121 MW; 9476BAC0BFC447 CRC64;
 SQ

Query Match 60.3%; Score 396.5; DB 2; Length 473;
 Best Local Similarity 65.6%; Pred. No. 5.9e-33;
 Matches 80; Conservative 14; Mismatches 21; Indels 7; Gaps 4;

QY 1 EVQLVESGGGLVQPGSLRLSCAASGYDFTYGMNVRQAQPKGLEWGMINTYGEPT 60
 DB 20 EVQLVESGGGLVQPGSLRLSCAASGYDFTYGMNVRQAQPKGLEWGMINTYGEPT 78
 QY 61 AADPKRRFTSLDTSKSTAYLQNSLRADPTAVYCAKPYGYTSHY---PFWGQ 116
 DB 79 YADSLQGRFTISRDNAKNSLYLQNSLRADPTAVYCAKPYH--TSPYPSFFDYWGQ 136
 QY 117 TL 118
 DB 137 IL 138

RESULT 14
 Q9HCC1
 ID Q9HCC1 PRELIMINARY; PRT; 112 AA.
 AC Q9HCC1;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Single chain Fv (fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB049915; BAB16829.1; -.
 DR HSP: P01783; IIGC.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003596; IG_V.
 DR SMART: SM00406; IG1; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;
 SQ

Query Match 60.1%; Score 395.5; DB 2; Length 112;
 Best Local Similarity 66.1%; Pred. No. 1.5e-33;
 Matches 78; Conservative 9; Mismatches 24; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVQPGSLRLSCAASGYDFTYGMNVRQAQPKGLEWGMINTYGEPT 60
 DB 1 EVQLVESGGGLVQPGSLRLSCAASGYDFTYGMNVRQAQPKGLEWGMINTYGEPT 60
 QY 61 AADPKRRFTSLDTSKSTAYLQNSLRADPTAVYCAKPYGYTSHYFPYWGQ 118
 DB 61 ADSVKGRTISRDNAKNSLYLQNSLRADPTAVYCAKPY-----ALDYWGQ 111

RESULT 15
 Q8WUK1
 ID Q8WUK1 PRELIMINARY; PRT; 613 AA.
 AC Q8WUK1;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE IGHM protein.
 OS Homo sapiens (Human).

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2005, 20:39:29 ; Search time 17.8553 Seconds

(without alignment)
635.867 Million cell updates/sec

Title: US-09-723-752b-7

Perfect score: 655
Sequence: 1 EVQLVDSGGGLVQPGGSLRL...YFHYGSSHWYFDVWGQSTL 118

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:1*
1: PIR1:1*
2: PIR2:1*
3: PIR3:1*
4: PIR4:1*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	433	66.1	119	2 S31107	Ig heavy chain - h
2	432	66.0	123	2 S31114	Ig heavy chain - h
3	432	66.0	125	2 S30531	Ig heavy chain V r
4	431.5	65.9	140	2 S70442	Ig heavy chain pre
5	431	65.8	138	2 S31666	Ig heavy chain V r
6	430.5	65.7	120	2 B42848	L6 mAb heavy chain
7	430	65.7	146	4 S33505	Ig heavy chain pre
8	430	65.6	131	2 S26792	Ig heavy chain V r
9	428	65.3	140	2 S31588	Ig heavy chain V r
10	426	65.0	123	2 S26794	Ig heavy chain V r
11	426	65.0	127	2 S38489	Ig heavy chain - h
12	424.5	64.8	128	2 S48797	Ig heavy chain V r
13	424	64.7	119	2 A53285	Ig heavy chain V a
14	423.5	64.7	115	2 S19678	Ig heavy chain V r
15	421	64.3	121	2 S15673	Ig heavy chain - h
16	421	64.3	142	2 S31686	Ig heavy chain V r
17	420	64.1	140	2 S19245	Ig heavy chain pre
18	419	64.0	121	2 S31104	Ig heavy chain V r
19	417.5	63.7	147	2 S37780	Ig heavy chain - h
20	417	63.7	121	2 S19666	Ig heavy chain V r
21	415.5	63.6	141	2 S31669	Ig heavy chain V r
22	415.5	63.4	114	2 D32967	Ig heavy chain V r
23	415	63.4	117	2 S36259	Ig heavy chain V r
24	415	63.4	119	2 S31108	Ig heavy chain - h
25	414.5	63.3	114	2 C32967	Ig heavy chain V r
26	414.5	63.3	122	2 E36005	Ig heavy chain V r
27	414.5	63.3	124	2 S27082	Ig heavy chain V r
28	414	63.2	119	2 D36005	Ig heavy chain V r
29	414	63.2	121	2 S31113	Ig heavy chain - h

30	414	63.2	160	2 S05271	Ig heavy chain pre
31	413.5	63.1	124	1 AVM551	Ig heavy chain V r
32	413	63.1	123	1 AVM551	Ig heavy chain V r
33	413	63.1	135	2 S31598	Ig heavy chain V r
34	413	63.1	143	2 S23624	Ig heavy chain V r
35	412.5	63.0	120	2 S48798	Ig heavy chain V r
36	412	62.9	119	2 C36005	Ig heavy chain V r
37	412	62.9	123	2 PLO017	Ig heavy chain V-D
38	410.5	62.7	119	2 S37453	Ig mu chain - huma
39	410	62.6	132	2 S31603	Ig heavy chain V r
40	409.5	62.5	122	2 S26789	Ig heavy chain V r
41	409.5	62.5	122	2 S31117	Ig heavy chain - h
42	408.5	62.4	114	2 S36280	Ig heavy chain V r
43	408.5	62.4	124	2 E30539	Ig heavy chain V r
44	408	62.3	117	2 S31109	Ig heavy chain - h
45	408	62.3	124	2 PH1404	Ig heavy chain V r

ALIGNMENTS

```
RESULT 1
S31107
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C/Accession: S31107
R/Raaphorst, F.M.; Timmer, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurma
Eur. J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A/Reference number: S31104; MUID:92111633; PMID:1730252
A/Accession: S31107
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-119 <RAA>
A/Cross-references: EMBL:X62955
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 66.1%; Score 433; DB 2; Length 119;
Matches 87; Conservative 8; Mismatches 19; Indels 4; Gaps 2;

QY 1 EVQLVDSGGGLVQPGGSLRLCAASGYPFTNYGMVWQAQPKGLEWYGMINTYGEPTY 60
DB 1 EVQLVDSGGGLVQPGGSLRLCAASGYPFTNYGMVWQAQPKGLEWYGMINTYGEPTY 60
QY 61 AADFRRTFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQSTL 118
DB 61 ADSVKGRTFTSRDNSKNTLYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQSTL 114

RESULT 2
S31114
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
R/Raaphorst, F.M.; Timmer, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurma
Eur. J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A/Reference number: S31104; MUID:92111633; PMID:1730252
A/Accession: S31114
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-123 <RAA>
A/Cross-references: EMBL:X62963
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>
```

Query Match 66.0%; Score 432; DB 2; Length 123;
 Best Local Similarity 71.2%; Pred. No. 2.3e-32;
 Matches 84; Conservative 7; Mismatches 27; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGSRLSCAASGTFRTNYGMNWVRQAPGKGLIEWGINTYGEPT 60
 DB 1 EVQLVESGGGLVQPGSRLSCAASGTFRTSYAMSWVRQAPGKGLIEWSAISGSGSTY 60
 QY 61 AADFKRRFTPSLDTSKSTAYLQNMNLRADTAIVYCAKYPHYGSSHWYFDVWGQGT 118
 DB 61 ADSVKGRTISRDNKNTLYLQNMNLRADTAIVYCAKASLYLRFLWEMFDVWGQGT 118

RESULT 3

S30531
 Ig heavy chain V region - human
 C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S30531
 R:Marlette, X.
 Submitted to the EMBL Data Library, October 1992

A:Reference number: S30520
 A:Accession: S30531
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-125 <MAR>
 A:Cross-references: UNIPROT:Q9UL91; EMBL:218317
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.0%; Score 432; DB 2; Length 123;
 Best Local Similarity 68.3%; Pred. No. 2.4e-32;
 Matches 82; Conservative 15; Mismatches 21; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVQPGSRLSCAASGTFRTNYGMNWVRQAPGKGLIEWGINTYGEPT 60
 DB 1 EVQLVESGGGLVQPGSRLSCAASGTFRTSYAMSWVRQAPGKGLIEWSAISGSGSTY 60
 QY 61 AADFKRRFTPSLDTSKSTAYLQNMNLRADTAIVYCAKYPHYGSSHWYFDVWGQGT 118
 DB 61 ADSVKGRTISRDNKNTLYLQNMNLRADTAIVYCAKASLYLRFLWEMFDVWGQGT 120

RESULT 4

S70442
 Ig heavy chain precursor V region (mu) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
 C:Accession: S70442
 R:Cuisinier, A.M.; Fougereau, M.; Tonnelie, C.
 Mol. Immunol. 29, 1363-1373, 1992

A:Title: IGM kappa/lambda BBV human B cell clone: an early step of differentiation of fe
 A:Reference number: S70442; MID:93024506; PMID:183635
 A:Accession: S70442
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-140 <CUI>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 65.9%; Score 431.5; DB 2; Length 140;
 Best Local Similarity 73.1%; Pred. No. 3e-32;
 Matches 87; Conservative 10; Mismatches 17; Indels 5; Gaps 4;

QY 1 EVOLVESGGGLVQPGSRLSCAASGTFRTNYGMNWVRQAPGKGLIEWGINTYGEPT 60
 DB 20 QVQLVESGGGLVQPGSRLSCAASGTFRTSYAMSWVRQAPGKGLIEWSAISGSGSTY 78
 QY 61 AADFKRRFTPSLDTSKSTAYLQNMNLRADTAIVYCAKYPHYGSSHWYFDVWGQGT 118

DB 79 YADSVKGRTISRDNKNTLYLQNMNLRADTAIVYCAK--DHIVGAT--YFDVWGQGT 134

RESULT 5

S31666
 Ig heavy chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S31666
 R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
 submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A:Reference number: S31585
 A:Accession: S31666
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-138 <CUI>
 A:Cross-references: EMBL:214202; NID:G30963; PIDN:CA78571.1; PID:G30964
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 65.8%; Score 431; DB 2; Length 138;
 Best Local Similarity 70.3%; Pred. No. 3.2e-32;
 Matches 83; Conservative 11; Mismatches 20; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVQPGSRLSCAASGTFRTNYGMNWVRQAPGKGLIEWGINTYGEPT 60
 DB 20 EVQLVESGGGLVQPGSRLSCAASGTFRTSYAMSWVRQAPGKGLIEWSAISGSGSTY 79
 QY 61 AADFKRRFTPSLDTSKSTAYLQNMNLRADTAIVYCAKYPHYGSSHWYFDVWGQGT 118
 DB 80 ADSVKGRTISRDNKNTLYLQNMNLRADTAIVYCAK---ARTGYTFDLWGQGT 133

RESULT 6

B42848
 L6 mab heavy chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: B42848; S33903
 R:Fell, H.P.; Gayle, M.A.; Yelton, D.; Lipsitch, L.; Schieven, G.L.; Marken, J.S.; Aruff
 J. Biol. Chem. 267, 15552-15558, 1992
 A:Title: Chimeric L6 anti-tumor antibody. Genomic construction, expression, and charact
 A:Reference number: A42848; MID:92348410; PMID:1635794

A:Accession: B42848
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-120 <FEU>
 A:Cross-references: GB:M0690; NID:G195065; PIDN:AA38146.1; PID:G195066
 A:Note: sequence extracted from NCBI Backbone (NCBI:109960, NCBI:109961)
 A:Accession: S33903
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-120 <FE2>
 A:Cross-references: EMBL:M90691
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 65.7%; Score 430.5; DB 2; Length 120;
 Best Local Similarity 65.8%; Pred. No. 3.1e-32;
 Matches 77; Conservative 20; Mismatches 17; Indels 3; Gaps 2;

QY 1 EVOLVESGGGLVQPGSRLSCAASGTFRTNYGMNWVRQAPGKGLIEWGINTYGEPT 60
 DB 1 QIQLVQSGPELKPKPESTYKISCKASGTFRTNYGMNWVRQAPGKGLIEWGINTYGOPT 60
 QY 61 AADFKRRFTPSLDTSKSTAYLQNMNLRADTAIVYCAKYPHYGSSHWYFDVWGQGT 117
 DB 61 AADFKRRFTPSLDTSKSTAYLQNMNLRADTAIVYCAKYPHYGSSHWYFDVWGQGT 114

RESULT 7

```

A:Accession: S31588
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <CUI>
C:Cross-references: EMBL:Z14200; NID:930957; PIDN:CAA78569.1; PID:930958
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 65.3%; Score 428; DB 2; Length 140;
Best Local Similarity 72.9%; Pred. No. 6.1e-32;
Matches 86; Conservative 9; Mismatches 21; Indels 2; Gaps 2;

OY 1 EVQLVESGGGLVPGGSLRLISCAASGYTFNMGWNRQAPGKGLEWGWINTYTGEPY 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 20 EVQLVESGGGLVPGGSLRLISCAASGYTFSSYASWRQAPGKGLEWASALISGGSTY 79
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 AADFKRFTFSLDTSKSTAYLQWNSLRADDTAVYYCAKPHYVSSHWYPDVWGQTL 118
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 80 ADSVKGRFTISRDSKNTLYLQWNSLRADDTAVYYCAK-DHDY-SNVIYFDYWGQTL 135
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
S26794
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C:Accession: S26794
R:Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fam
A:Reference number: S26786; MUID:92111632; PMID:11730251
A:Accession: S26794
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-123 <MOR>
C:Cross-references: EMBL:X61011
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 65.0%; Score 426; DB 2; Length 123;
Best Local Similarity 68.4%; Pred. NO. 8.2e-32;
Matches 80; Conservative 14; Mismatches 23; Indels 0; Gaps 0;

OY 1 EVQLVESGGGLVPGGSLRLISCAASGYTFNMGWNRQAPGKGLEWGWINTYTGEPY 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVQLVESGGGLVPGGSLRLISCAASGYTFSSYASWRQAPGKGLEWASALISGGSTY 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 AADFKRFTFSLDTSKSTAYLQWNSLRADDTAVYYCAKPHYVSSHWYPDVWGQGT 117
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 ADSVKGRFTISRDAKNSLYLQWNSLRADDTAVYYCARSIKYDENVYGMQVWGQGT 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
S38489
Ig heavy chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38489
R:Markes, J.D.; Ouehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe,
submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from a
A:Reference number: S38488
A:Accession: S38489
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-127 <MAR>
C:Cross-references: EMBL:Z23028; NID:9414025; PIDN:CAA80563.1; PID:9414026
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

```

Query Match 65.0%; Score 426; DB 2; Length 127;
 Best Local Similarity 69.9%; Pred. No. 8.4e-32;
 Matches 86; Conservative 11; Mismatches 21; Indels 6; Gaps 3;

Qy 1 EVOLVESGGGLVQPGSLRLSCAASGTFPTNYGMWVRQAPGKGLIEWGINTYTGEPY 60
 Db 1 QVQLVQSGGAVVQPGSLRLSCAASGTFPTSYAMSVRQAPGKGLIEWGAIISGSGSTY 60

Qy 61 AADFRRTFSLDTSKSTAYLQWNSLRADTAIVYCAK---YF--HYGSSHWY-FDWG 114
 Db 61 ADVKGRFTISRDNKNTLYLQWNSLRADTAIVYCAKGGPPADYDSSGYSGFDYWG 120

Qy 115 QGTL 118
 Db 121 QGTL 124

RESULT 12

ig heavy chain V region (antl-Sm, VH3/Dxp4/JHe) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999

C/Accession: S48797; S26893

R/Maimoudi, M.; Edwards, J.; Cairns, E.; Bell, D.

submitted to the EMBL Data Library, October 1994

A/Description: Molecular characterization of natural human anti-Sm autoantibodies.

A/Reference number: S48797

A/Accession: S48797

A/Molecule type: mRNA

A/Residues: 1-128 <MAN>

A/Cross-references: EMBL:246379; NID:9587147; PIDN:CAA86512.1; PID:91340168

R/Tomlinson, I.M.; Walter, G.; Marke, J.D.; Llewellyn, M.B.; Winter, G.

J.Mol. Biol. 227, 776-798, 1992

A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A/Reference number: S26885; MUID:93021117; PMID:1404388

A/Accession: S26893

A/Molecule type: DNA

A/Residues: 1-98 <TOM>

A/Cross-references: EMBL:212350; NID:932922; PIDN:CAA78220.1; PID:932923

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: heterotetramer; Immunoglobulin

F.15-98/Domain: Immunoglobulin homology <IMM>

Query Match 64.8%; Score 424.5; DB 2; Length 128;
 Best Local Similarity 69.9%; Pred. No. 1.2e-31;
 Matches 86; Conservative 11; Mismatches 19; Indels 7; Gaps 3;

Qy 1 EVOLVESGGGLVQPGSLRLSCAASGTFPTNYGMWVRQAPGKGLIEWGINTYTGEPY 60
 Db 1 QVQLVQSGGAVVQPGSLRLSCAASGTFPTSYAMSVRQAPGKGLIEWGINTYTGEPY 59

Qy 61 AADFRRTFSLDTSKSTAYLQWNSLRADTAIVYCAKPHYGSSHWYF-----DWG 114
 Db 60 YADVKGRTISRDNKNTLYLQWNSLRADTAIVYCAADNYDSSGYTYYGMDWG 119

Qy 115 QGTL 117
 Db 120 QGTL 122

RESULT 13

ig heavy chain V and J regions, monoclonal antibody SCRT.M8.1 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000

C/Accession: A53285

R/Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.

Mol. Immunol. 28, 1063-1072, 1991

A/Title: Molecular characterization of monoclonal anti-steroid antibodies: primary struc

and their pH-reactivity profiles

A/Reference number: A53285; MUID:92017897; PMID:1922102

A/Accession: A53285

A/Status: Preliminary

A/Molecule type: DNA; protein

A/Residues: 1-119 <SAM>

A/Cross-references: GB:D12766; NID:9220595; PIDN:BA02228.1; PID:9220596

A/Note: Sequence extracted from NCBI Backbone (NCBI:63277, NCBI:63299)

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: heterotetramer; Immunoglobulin

F.15-98/Domain: Immunoglobulin homology <IMM>

Query Match 64.7%; Score 424; DB 2; Length 119;
 Best Local Similarity 66.1%; Pred. No. 1.2e-31;
 Matches 78; Conservative 16; Mismatches 18; Indels 6; Gaps 2;

Qy 1 EVOLVESGGGLVQPGSLRLSCAASGTFPTNYGMWVRQAPGKGLIEWGINTYTGEPY 60
 Db 1 QVQLVQSGGLKGGTIVYKISCKASGTFPTNYGMWVRQAPGKGLIEWGINTYTGEPY 60

Qy 61 AADFRRTFSLDTSKSTAYLQWNSLRADTAIVYCAKPHYGSSHWY-FDWGQGT 117
 Db 61 ADFKGRFASLETSTASTAYLQINDLNEDTATYFCAR-----GNRVYAMDYWGQGT 113

RESULT 14

ig heavy chain V region (M-T408) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004

C/Accession: S19968

R/Weissenhorn, W.; Rietmueler, G.; Weiss, E.M.; Rieber, E.P.

submitted to the EMBL Data Library, March 1992

A/Description: Structural characterization of CD4 mAb.

A/Reference number: S19963

A/Accession: S19968

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-115 <WBI>

A/Cross-references: UNIPROT:Q921A6; EMBL:X65089

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: heterotetramer; Immunoglobulin

F.10-93/Domain: Immunoglobulin homology <IMM>

Query Match 64.7%; Score 423.5; DB 2; Length 115;
 Best Local Similarity 67.9%; Pred. No. 1.3e-31;
 Matches 76; Conservative 15; Mismatches 18; Indels 3; Gaps 1;

Qy 6 EGGGLVQPGSLRLSCAASGTFPTNYGMWVRQAPGKGLIEWGINTYTGEPYADPK 65
 Db 1 QSGPELKTPESTVTKISCAASGTFPTNYGMWVRQAPGKGLIEWGINTYTGEPYADPK 60

Qy 66 RRTFSLDTSKSTAYLQWNSLRADTAIVYCAKPHYGSSHWYFDWGQGT 117
 Db 61 GRFASLETSTASTAYLQINDLNEDTAVYFCARGPYRFS---FDYWGQGT 109

RESULT 15

ig heavy chain - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000

C/Accession: S15673

R/Knight, G.B.; Agnello, V.; Bonagura, V.; Barnes, J.L.; Panke, D.J.; Zhang, Q.X.

J. Exp. Med. 178, 1903-1911, 1993

A/Title: Human rheumatoid factor cross-identity. IV. Studies on WA Xid-positive IGM w1

linc from the 17.10 and G6 Xids

A/Reference number: S15673; MUID:94065558; PMID:8245772

A/Accession: S15673

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-121 <RES>

A/Cross-references: GB:M07268; NID:9186197; PIDN:AAC37536.1; PID:9186198

C/Genetics:

A/Gene: GDB:IGM

A/Cross-references: GDB:120086, OMIM:147020

A/Map position: 14q32.33-14q32.33

C:Superfamily: immunoglobulin V region; immunoglobulin homology
F,15-98/Domain: immunoglobulin homology <IWM>

Query Match 64.3%; Score 421; DB 2; Length 121;
Best Local Similarity 70.3%; Pred. No. 2.3e-31;
Matches 83; Conservative 8; Mismatches 25; Indels 2; Gaps 1;

QY	1	EVQLVESGGGLVQPQGGSLRLGCAAGYFTNYGMWVROAPGKGLEWYGMINTYGEPTY	60
		:	
DB	1	EVQLVESGGGLVQPQGGSLRLSCTASGFTPTSGMSWROAPGKGLEWVSAISGGGSTYY	60
		:	
QY	61	AADFRRFTPSLDTSKSTAYLQMSLRAEDFAVYCAKYPHYGSSHWYFDVWGQGTL	118
		:	
DB	61	ADSVKGRFTISRDNKNTLYLQMSLRAEDFAVYCAAPRHAGSP--YDYMGGTL	116
		:	

Search completed: March 14, 2005, 21:08:50
Job time : 18.8553 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2005, 20:32:33 ; Search time 82.807 Seconds

(without alignments)
729.713 Million cell updates/sec

Title: US-09-723-752b-7

Perfect score: 655
Sequence: 1 EVLVESGGGLVQPGGSLRL.....YPHYGSSHWYFDVWGQCTL 118Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	425.5	65.0	475	2	Q6MZ06
2	420	64.1	597	2	Q96BB9
3	419.5	64.0	241	2	Q921A6
4	415.5	63.4	118	2	Q9UL91
5	415.5	63.4	122	1	HV21_MOUSE
6	413	63.1	123	1	HV18_MOUSE
7	410	62.6	113	2	Q9UL50
8	409	62.4	123	1	HV19_MOUSE
9	405.5	61.9	606	2	Q6GMT2
10	405	61.8	120	1	HV3E_HUMAN
11	404.5	61.6	573	2	Q8WU38
12	403.5	61.6	613	2	Q8WUK1
13	402.5	61.5	473	2	Q6MZV7
14	402	61.4	123	1	HV23_MOUSE
15	401.5	61.3	112	2	Q9HCT1
16	401	61.2	123	1	HV22_MOUSE
17	401	61.2	472	2	Q6N089
18	400	61.1	240	2	Q6SZC9
19	399	60.9	470	2	Q6PUJ4
20	398.5	60.8	122	1	HV20_MOUSE
21	397.5	60.7	544	2	Q6PUJ5
22	397	60.6	478	2	Q6P181
23	397	60.6	487	2	Q80Z17
24	395	60.3	464	2	Q6MZU6
25	393.5	60.1	147	2	Q9Y509
26	393	60.0	121	2	Q9UL71
27	393	60.0	499	2	Q8NSK4
28	388	59.2	115	1	HV3D_HUMAN
29	388	59.2	123	1	HV24_MOUSE
30	387.5	59.2	122	1	HV3G_HUMAN
31	387.5	59.2	483	2	Q6MZX9

32	387	59.1	125	2	Q6P1L0	Q6P1L0 homo sapien
33	386	58.9	485	2	Q6PDB8	Q6PDB8 mus musculus
34	383.5	58.5	479	2	Q6MZV6	Q6MZV6 homo sapien
35	383.5	58.5	487	2	Q6ZVX0	Q6ZVX0 homo sapien
36	382	58.3	493	2	Q6GMX2	Q6GMX2 homo sapien
37	381.5	58.2	122	2	Q9UL84	Q9UL84 mus musculus
38	381	58.2	470	2	Q7TMC1	Q7TMC1 mus musculus
39	380	58.0	121	1	HV3J_HUMAN	P01771 homo sapien
40	379.5	57.9	119	1	HV38_MOUSE	P01808 mus musculus
41	379	57.9	123	1	HV25_MOUSE	P01794 mus musculus
42	378.5	57.8	118	2	Q9UL72	Q9UL72 homo sapien
43	378.5	57.8	119	1	HV37_MOUSE	P01807 mus musculus
44	377	57.6	116	2	Q9UL53	Q9UL53 homo sapien
45	376.5	57.5	136	1	HV16_MOUSE	P01763 mus musculus

ALIGNMENTS

RESULT 1

Q6MZ06 PRELIMINARY; PRT; 475 AA.

AC Q6MZ06; Q6MZ06; (REMBLrel. 27, Created)

DT 05-JUL-2004 (REMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (REMBLrel. 27, Last annotation update)

DE Hypothetical protein DKFZp686G1190.

GN Name=DKFZp686G1190;

OS Homo sapiens (Human);

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Human esophagus tumor;

RG The German Human cDNA Consortium;

RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,

RA Han M., Wiemann S.;

RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BX640947; CAE45972.1; -.

DR HSBP; P01861; IADQ.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG-cl.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_v.

DR Pfam; PF07654; C1-sect; 3.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGcl; 3.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 4.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.

KW Hypothetical protein.

SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F488E CRC64;

Query Match 65.0%; Score 425.5; DB 2; Length 475;

Best Local Similarity 71.3%; Pred. No. 2.7e-36;

Matches 87; Conservative 12; Mismatches 18; Indels 5; Gaps 4;

QY 1 EVLVESGGGLVQPGGSLRLCAAGYTFNYGNWVROAPGKLEWVGNINTYGEPTY 60

DB 20 EVLVESGGGLVQPGGSLRLSCAAGTFPNYGMWVROAPGKLEWVSGISS-SGVNTY 78

QY 61 AAD-FKRRFFSLDTSKSYVLDONSIRADTVAYYCAK--YPHYGSS-SHWYFDVWGQ 116

DB 79 YADSVKGRFTISDITNTLYLQMHSIRADTVAYYCARADYRDYQVSPAYWYFDVWG 138

QY 117 TL 118

DB 139 TL 140

RESULT 2

```

Q96BB9          PRELIMINARY;      PRT;      597 AA.
ID   Q96BB9
AC   Q96BB9
DT   01-DEC-2001 (TREMBLrel. 19, Created)
DT   01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE   IGM protein. (Human).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX   NCBI_TaxId=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Maruina K., Farmer A.A., Rubin G.W., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Grouman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Timwood J., Schmitt J., Myers R.M., Butterfield Y.S.,
RA   Krzywniński M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA   Jones S.U., Maiz M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences."
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RA   Strauberg R.;
RA   EMBL; BC015760; AAH15760.1; -.
RA   PIR; S05271; S05271.
RA   PIR; S24260; S24260.
RA   HSSP; P01861; IADQ.
RA   InterPro; IPR007110; IG-1like.
RA   InterPro; IPR003597; IG-cl.
RA   InterPro; IPR003006; IG_MHC.
RA   InterPro; IPR003596; IG_v.
RA   Pfam; PF07654; CI-sect; 4.
RA   SMART; SM00406; IGV; 1.
RA   PROSITE; PS50835; IG_LIKE; 5.
RA   PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ   SEQUENCE 597 AA; 65039 MW; 4FC3AD8CE263D9 CRC64;

Query Match      64.1%; Score 420; DB 2; Length 597;
Best Local Similarity 70.0%; Pred. No. 1,3e-35;
Matches 84; Conservative 8; Mismatches 26; Indels 2; Gaps 1;

Qy 1 EVLVESGGGLVQPGGSLRLSCAASGTFPTNYGMVWQAPGKGLRWGINTYGEPT 60
Db 20 EVQLVESGGGLVQPGGSLRLSCAASGTFPTNYGMVWQAPGKGLRWGINTYGEPT 79
Qy 61 AADPKRRTFSLDTSKSTAYLQMSLRADDTAVYCAKYPHYGSSHWYF--DWGGQ 118
Db 80 ADVVGRFTISDNRDLTYLQMSLRADDTAVYCAKYPHYGSSHWYF--DWGGQ 139

RESULT 3
ID   Q921A6          PRELIMINARY;      PRT;      241 AA.
AC   Q921A6;
DT   01-DEC-2001 (TREMBLrel. 19, Created)
DT   01-DEC-2001 (TREMBLrel. 19, Last sequence update)

```

```

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Anti-CEA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   MEDLINE=98170165; PubMed=9509426;
RA   Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA   Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT   "Cloning and characterization of cDNAs encoding VH and VL of a
RT   monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT   generation of a single-chain Fv molecule (scFv).";
RL   Mol. Cells 7:816-819(1997).
RX   EMBL; U88067; AAB48044.1; -.
DR   PIR; S19965; S19965.
DR   PIR; S19967; S19967.
DR   PIR; S19968; S19968.
DR   PIR; S26325; S26325.
DR   HSSP; P01607; LBWV.
DR   SMART; SM00406; IGV; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
FT   NON_TER 1
FT   NON_TER 241
SQ   SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match      64.0%; Score 419.5; DB 2; Length 241;
Best Local Similarity 65.0%; Pred. No. 5.5e-36;
Matches 76; Conservative 18; Mismatches 18; Indels 5; Gaps 1;

Qy 1 EVLVESGGGLVQPGGSLRLSCAASGTFPTNYGMVWQAPGKGLRWGINTYGEPT 60
Db 1 QVRLQDSGPELVKKGKGVTKISCRASGTFPTDYGMVWQAPGKGLRWGINTYGEPT 60
Qy 61 AADPKRRTFSLDTSKSTAYLQMSLRADDTAVYCAKYPHYGSSHWYFEDWGQGT 117
Db 61 AADPKRRTFSLDTSKSTAYLQMSLRADDTAVYCAKYPHYGSSHWYFEDWGQGT 112

RESULT 4
ID   Q9UL91          PRELIMINARY;      PRT;      118 AA.
AC   Q9UL91;
DT   01-MAY-2000 (TREMBLrel. 13, Created)
DT   01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX   NCBI_TaxId=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus."
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
RX   EMBL; AF035023; AAD56259.1; -.
DR   PIR; PH0875; PH0875.
DR   PIR; S21205; S21205.
DR   PIR; S30531; S30531.
DR   HSSP; P01783; IIGC.
DR   InterPro; IPR007110; IG-1like.
DR   InterPro; IPR003596; IG_v.
RA   SMART; SM00406; IGV; 1.
RA   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER 1
FT   NON_TER 118
SQ   SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

```


Query Match 63.4%; Score 415.5; DB 2; Length 118;
 Best Local Similarity 68.6%; Pred. No. 6.6e-36;
 Matches 81; Conservative 12; Mismatches 20; Indels 5; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGTFYFNMGMMVRAQAPGKLEWY---GWINTYTG 60
 DB 1 EVOLVESGGGLVOPGSLRLSCAASGTFSSYMMWVRQAPGKLEWYSISITITITY 60
 QY 61 AADPKRRTFSLDTSKSTAYIQMNSLRADETAVYCAKYPHYGSSHWYFDVWGGL 118
 DB 61 ADVYKGRFTIRSDNAKNSLYIQMNSLRADETAVYCAR-----GDSSEAFDWGGL 113

RESULT 5

HV12_MOUSE
 ID HV12_MOUSE STANDARD; PRT; 122 AA.

AC P01790;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig heavy chain V region M511.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX NCBI_TaxId=10090;
 RN [1]

RP SEQUENCE.
 RX MEDLINE=81054880; PubMed=6776528;
 RA Robinson E.A., Appella E.;
 RT "Complete amino acid sequence of a mouse immunoglobulin alpha chain
 (MOPC 511)."
 RL Proc. Natl. Acad. Sci. U.S.A. 77:4909-4913(1980).
 CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that
 binds phosphorylcholine.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR HSP; P01789; IMCP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 114
 FT NON_TER 122 122
 FT SEQUENCE 122 AA; 13652 MW; 9F4837731EAS0207 CRC64;
 SQ

Query Match 63.4%; Score 415.5; DB 1; Length 122;
 Best Local Similarity 66.9%; Pred. No. 6.8e-36;
 Matches 81; Conservative 13; Mismatches 18; Indels 9; Gaps 3;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGTFYFNMGMMVRAQAPGKLEWY---GWINTYTG 56
 DB 1 EVOLVESGGGLVOPGSLRLSCATSGTFSDPYEMWVRQAPGKLEWIAASRNKANDYTT 60
 QY 57 EPTAADPKRRTFSLDTSKSTAYIQMNSLRADETAVYCAKYPHYGSSHWYFDVWGGL 116
 DB 61 E-YSASVKGKRFIVSRDTSOSILYIQMNSLRADETAVYCAR---DYGSSYWFVWGAG 115
 QY 117 T 117
 DB 116 T 116

RESULT 6

HV18_MOUSE
 ID HV18_MOUSE STANDARD; PRT; 123 AA.

AC P01787;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig heavy chain V regions TIPC 15/S107/HPCM1/HPCM2/HPCM3.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX NCBI_TaxId=10090;
 RN [1]

RP SEQUENCE (TEPC 15).
 RX MEDLINE=76222762; PubMed=819932;
 RA Rudikoff S., Potter M.;
 RT "Size differences among immunoglobulin heavy chains from
 phosphorylcholine-binding proteins."
 RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
 RN [2]

RP SEQUENCE FROM N.A. (H107).
 RX MEDLINE=80199926; PubMed=6769593; DOI=10.1016/0092-8674(80)90089-6;
 RA Early P., Huang H., Davis M., Calame K., Hood L.;
 RT "An immunoglobulin heavy chain variable region gene is generated from
 three segments of DNA: VH, D and JH."
 RL Cell 19:981-992(1980).
 RN [3]

RP SEQUENCE (S107).
 RX MEDLINE=76110488; PubMed=813561;
 RX DOI=10.1146/annurev.ge.09.120175.001513;
 RA Rudikoff S., Barstad P., Potter M., Hood L.;
 RL Unpublished results, cited by:
 RL Hood L., Campbell J.H., Eskin S.C.R.;
 RL Annu. Rev. Genet. 9:305-353(1975).
 RN [4]

RP SEQUENCE (HPCM1, HPCM2 AND HPCM3).
 RX MEDLINE=81197602; PubMed=7231520;
 RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
 RT "IgG antibodies to phosphorylcholine exhibit more diversity than their
 IgM counterparts."
 RL Nature 291:28-34(1981).
 CC -1- MISCELLANEOUS: All those sequence appears to be identical.
 CC -1- MISCELLANEOUS: These chains were isolated from myeloma and
 hybridoma proteins that bind phosphorylcholine.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A93804; AVMSSTS.
 DR HSP; P01789; IMCP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Direct protein sequencing; Hybridoma; Immunoglobulin V region.
 FT DOMAIN 1 114
 FT NON_TER 123 123
 FT SEQUENCE 123 AA; 13777 MW; 9D58086DE12F7000 CRC64;
 SQ

Query Match 63.1%; Score 413; DB 1; Length 123;
 Best Local Similarity 66.9%; Pred. No. 1.3e-35;
 Matches 81; Conservative 12; Mismatches 20; Indels 8; Gaps 3;

QY 1 EVOLVESGGGLVOPGSLRLSCAASGTFYFNMGMMVRAQAPGKLEWY---GWINTYTG 56
 DB 1 EVOLVESGGGLVOPGSLRLSCATSGTFSDPYEMWVRQAPGKLEWIAASRNKANDYTT 60
 QY 57 EPTAADPKRRTFSLDTSKSTAYIQMNSLRADETAVYCAKYPHYGSSHWYFDVWGGL 116
 DB 61 E-YSASVKGKRFIVSRDTSOSILYIQMNSLRADETAVYCAR---DYGSSYWFVWGAG 116
 QY 117 T 117
 DB 117 T 117

RESULT 7

O9UL90
 ID O9UL90 PRELIMINARY; PRT; 113 AA.

AC O9UL90;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region


```

Db      20 QVQLVESGGGLVPGGSLRLSCAASGFTPSDYMIRCAAPGKLEWVSISSTSYNY 79
Qy      61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAK-----YPHYG 104
Db      80 ADSVKGRTTISRDNKNSLYLQMSLRADTAIVYCAKRGNGIAAGRVVYADYVYGG 139
Qy      105 SSHWYFDVWGQGT 117
Db      140 -----MDVWGQGT 147

RESULT 10
HV3E HUMAN STANDARD; PRT; 120 AA.
AC P01766;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-II region BRO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71117674; PubMed=65324; DOI=10.1016/0019-2791(76)90271-8;
RA Capra J.D., Hopper J.E.;
RT "Comparative studies on monocytic IgM lambda and IgG kappa from an
RT individual patient. III. The complete amino acid sequence of the VH
RT region of the IgM paraprotein."
RL Immunohistochemistry 13:995-999(1976).
CC -1- MISCELLANEOUS: This chain was obtained from IgM isolated from the
CC serum of a patient with malignant lymphoma of the Waldenstrom
CC type.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02049; M3HUBW.
DR HSBP; P01783; 11GC.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 111
FT NON TER 120
SQ SEQUENCE 120 AA; 13327 MW; D3F0428F7C2B6410 CRC64;

Query Match 61.8%; Score 405; DB 1; Length 120;
Best Local Similarity 66.1%; Pred. No. 8.6e-35;
Matches 84; Conservative 7; Mismatches 20; Indels 16; Gaps 3;

Qy      1 EVOLVESGGGLVPGGSLRLSCAASGFTPSDYMIRCAAPGKLEWVSISSTSYNY 60
Db      1 EVOLVESGGGLVPGGSLRLSCAASGFTPSDYMIRCAAPGKLEWVSISSTSYNY 59
Qy      61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAK-----HYGSSHWYFD 111
Db      60 ADSVKGRTTISRDNKNSLYLQMSLRADTAIVYCAKRGNGIAAGRVVYADYVYGG 113
Qy      112 VMGQGT 118
Db      114 VMGQGT 120

RESULT 11
Q8WU38 PRELIMINARY; PRT; 573 AA.
AC Q8WU38;
DT 01-MAR-2002 (TREMBLrel. 20, Created)

```

```

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Meng J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Uedeli T.B., Toshiyuki S., Carninci P., Prange C.,
RA Baha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosa S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalski U., Smallus D.E., Schnerch A., Schain J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Primary B-Cells;
RA Straubeberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021276; AAH21276.1; -.
DR PIR; S21205; S21205.
DR PIR; S30532; S30532.
DR HSBP; P18529; 118K.
DR Pfam; PF07654; C1-sect; 2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 573 AA; 62967 MW; FD07234403AC530 CRC64;

Query Match 61.8%; Score 404.5; DB 2; Length 573;
Best Local Similarity 65.9%; Pred. No. 5.5e-34;
Matches 81; Conservative 11; Mismatches 20; Indels 11; Gaps 2;

Qy      1 EVOLVESGGGLVPGGSLRLSCAASGFTPSDYMIRCAAPGKLEWVSISSTSYNY 60
Db      20 EVOLVESGGGLVPGGSLRLSCAASGFTPSDYMIRCAAPGKLEWVSISSTSYNY 79
Qy      61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAK-----PHYGSSHWYFD 114
Db      80 ADSVKGRTTISRDNKNSLYLQMSLRADTAIVYCAKRGNGIAAGRVVYADYVYGG 134
Qy      115 QGT 117
Db      135 QGT 137

RESULT 12
Q8WU38 PRELIMINARY; PRT; 613 AA.
AC Q8WU38;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE IGHM protein.

```

```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2238625; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strauberg R.L.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020240; AAH20240.1; -
DR PIR; F36005; F36005.
DR PIR; G36005; G36005.
DR PIR; PH1642; PH1642.
DR PIR; PH1643; PH1643.
DR PIR; PH1645; PH1645.
DR PIR; PH1646; PH1646.
DR PIR; PL0098; PL0098.
DR PIR; PL0120; PL0120.
DR PIR; S15590; S15590.
DR PIR; S31116; S31116.
DR PIR; S31119; S31119.
DR PIR; S70442; S70442.
DR HSSP; P01861; IADQ.
DR Pfam; PF07654; Cl-sect; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 613 AA; 67295 MW; 60C7F5950671E315 CRC64;

Query Match 61.6%; Score 403.5; DB 2; Length 613;
Best Local Similarity 66.9%; Pred. No. 7.6e-34;
Matches 83; Conservative 10; Mismatches 16; Indels 15; Gaps 4;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYPFTNGMVRWROAPGKGLIEWGINTYGEPTT 60
DB 20 QVQLVESGGLVQPGGSLRLSCAASGFTFSYGMHWROAPGKGLIEWAVI-SYDGSNKY 78
QY 61 AAD-FKRFTFSLDTSKSTAYLQNNSLRAEDTAVYYCAKPHYYSRHW-----YEDWG 114
DB 79 YADSLQGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCAK-----DMSGEVTFDIWG 130
QY 115 QGTL 118
DB 131 QGTM 134
RESULT 13
ID Q6M2V7 PRELIMINARY; PRT; 473 AA.

```

```

AC Q6M2V7;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C11235.
GN Name=DKFZp686C11235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human small intestine;
RG The German Human cDNA Consortium;
RA Bloecher H., Boecher M., Meves H.W., Weil B., Amid C., Oeanger A.,
RA Pobo G., Han M., Wilmann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640853; CAB45920.1; -
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003597; IG_CL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; Cl-sect; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 52121 MW; 9476EAE4C0BFC447 CRC64;

Query Match 61.5%; Score 402.5; DB 2; Length 473;
Best Local Similarity 65.6%; Pred. No. 7.3e-34;
Matches 80; Conservative 16; Mismatches 19; Indels 7; Gaps 4;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYPFTNGMVRWROAPGKGLIEWGINTYGEPTT 60
DB 20 EIQLVESGGGLVQPGGSLRLSCAASGFTFSFENWROAPGKGLIEWLSY-TSGNTIV 78
QY 61 AAD-FKRFTFSLDTSKSTAYLQNNSLRAEDTAVYYCAKPHYYSRHW-----EDWGCG 116
DB 79 YADSLQGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCAKQNEH--TSPWYVSFDYWGCG 136
QY 117 TL 118
DB 137 IL 138
RESULT 14
ID HV23_MOUSE STANDARD; PRT; 123 AA.
AC P01792;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V region HPC8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "IgG antibodies to phosphorylcholine exhibit more diversity than their
RT IGM counterparts.";
RL Nature 291:29-34 (1981).
CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC binds phosphorylcholine.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; E93256; AVMSH8.

```

DR HSSP; P01789; IMCP.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PSS0835; IG LIKE; 1.
 DR Direct protein sequencing; Hybridoma; Immunoglobulin V region.
 FT DOMAIN 1 114
 FT NON TER 123 123
 SQ SEQUENCE 123 AA; 13879 MW; 4559D3106CAF7D8D CRC64;

Query Match 61.4%; Score 402; DB 1; Length 123;
 Best Local Similarity 65.3%; Pred. No. 1.8e-34;
 Matches 79; Conservative 12; Mismatches 22; Indels 8; Gaps 3;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGTFITNYGMWVRQAPGKGLEWVGINT---YTG 56
 DB 1 EVQLVESGGGLVPGGSLRLSCAASGTFITNYGMWVRQAPGKGLEWVGINT---YTG 60

QY 57 EPTVAADFKRFTSLTSTAYLQNSLRADPTAVYYCAKPHYGSSHWYFDVWGQG 116
 DB 61 E--YSAVKGKRFIVSRDTSQILYLOMNALEADTAIYYCAR--DYGSRIWYFDVWGAG 116

QY 117 T 117
 DB 117 T 117

RESULT 15

Q9HCCI PRELIMINARY; PRT; 112 AA.

AC Q9HCCI;
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Single chain Fv (Fragment).
 OS Homo sapiens (Human).
 OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.,
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB049915; BAB16829.1; -.
 DR HSSP; P01789; IIGC.
 DR InterPro; IPR007110; IG-like.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PSS0835; IG LIKE; 1.
 FT NON TER 1 1
 FT NON TER 112 112
 SQ SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;

Query Match 61.3%; Score 401.5; DB 2; Length 112;
 Best Local Similarity 66.1%; Pred. No. 1.9e-34;
 Matches 78; Conservative 11; Mismatches 22; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGTFITNYGMWVRQAPGKGLEWVGINTYTGEPY 60
 DB 1 EVQLVESGGGLVPGGSLRLSCAASGTFITNYGMWVRQAPGKGLEWVGINTYTGEPY 60
 QY 61 AADFKRFTSLTSTAYLQNSLRADPTAVYYCAKPHYGSSHWYFDVWGQGTLL 118
 DB 61 ADSVKGKRFIVSRDTSQILYLOMNALEADTAIYYCAR-----RRYALDYWGQGTLL 111

Search completed: March 14, 2005, 20:49:18
 Job time : 84.807 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2005, 20:21:17 ; Search time 88.0482 Seconds
(without alignments)
483.186 Million cell updates/sec

Title: US-09-723-752B-8

Perfect score: 576

Sequence: 1 DIQMTQSPSSLSASVGRVT.....YSTVPTFGQCTKVEIKRTV 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	576	100.0	110	3	AAB05897 Humanised
2	576	100.0	110	3	AAB13376 F(ab)-12
3	576	100.0	237	8	ADQ90721 Anti-VEGF
4	573	99.5	110	2	AAW70677 Anti-VEGF
5	573	99.5	110	2	AAW70687 Anti-VEGF
6	573	99.5	110	3	AAB13380 Anti-VEGF
7	573	99.5	110	5	ABP61256 Humanised
8	573	99.5	110	5	ABP61246 Humanised
9	573	99.5	214	7	ADC26154 Parent an
10	573	99.5	237	5	ABB81107 Anti-VEGF
11	573	99.5	237	5	ABP51952 Plasmid P
12	573	99.5	237	8	ADQ14128 Plasmid P
13	573	99.5	237	8	ADQ14131 Plasmid P
14	573	99.5	237	8	ADQ90703 Anti-VEGF
15	573	99.5	237	8	ADQ90701 Anti-VEGF
16	573	99.5	237	8	ADQ90705 Anti-VEGF
17	573	99.5	237	8	ADQ90709 Anti-VEGF
18	573	99.5	237	8	ADQ90723 Anti-VEGF
19	573	99.5	237	8	ADQ90707 Anti-VEGF
20	570	99.0	110	2	AAW70675 Anti-VEGF
21	570	99.0	110	5	ABP61244 Humanised
22	567	98.4	108	5	AAW70618 Anti-VEGF
23	567	98.4	108	5	ABP61187 Humanised
24	567	98.4	108	8	ADG31782 V(L) doma
25	567	98.4	108	8	ADG31768 V(L) doma

26	567	98.4	108	8	ADG31893	ADG31893 V(L) prot
27	567	98.4	110	2	AAW70673	AAW70673 Anti-VEGF
28	567	98.4	110	5	ABP61242	ABP61242 Humanised
29	567	98.4	237	2	AAW70703	AAW70703 Protein e
30	567	98.4	650	5	ABP61241	ABP61241 Phage-dls
31	564	97.9	108	8	ADG31770	ADG31770 V(L) doma
32	561	97.4	108	2	AAW70696	AAW70696 Anti-VEGF
33	561	97.4	108	5	ABP61265	ABP61265 Humanised
34	559	97.0	107	2	AAW68023	AAW68023 Variable
35	559	97.0	107	2	AAW70622	AAW70622 Humanised
36	559	97.0	107	5	ABP61192	ABP61192 Humanised
37	556	96.5	107	2	AAW68805	AAW68805 Variable
38	556	96.5	107	2	AAW70625	AAW70625 Humanised
39	556	96.5	107	2	AAW61194	AAW61194 Humanised
40	556	96.5	214	7	ADC26157	ADC26157 Anti-VEGF
41	555	96.4	214	7	ADC26156	ADC26156 Anti-VEGF
42	554	96.2	110	2	AAW70685	AAW70685 Anti-VEGF
43	554	96.2	110	2	AAW70681	AAW70681 Anti-VEGF
44	554	96.2	110	2	AAW70683	AAW70683 Anti-VEGF
45	554	96.2	110	2	AAW70679	AAW70679 Anti-VEGF

ALIGNMENTS

RESULT 1	
AAB05897	standard; peptide; 110 AA.
ID	AAB05897
AC	AAB05897;
XX	
DT	17-OCT-2000 (first entry)
XX	
DE	Humanised anti-VEGF antibody F(ab)-12 light chain variable domain.
XX	
KW	Humanised, F(ab)-12, light chain variable domain; antibody variant;
KW	phage display; randomised library; cytosolic; antiarteriosclerotic;
KW	antiproliferative; antidiabetic; antiinflammatory; antiarteriosclerotic;
KW	vascular endothelial growth factor; VEGF; breast cancer; lung cancer;
KW	retinoblastoma; rheumatoid arthritis; psoriasis; atherosclerosis;
KW	diabetic retinopathy; complementarily determining region; CDR.
XX	
OS	Homo sapiens.
XX	
XX	Synthetic.
XX	
PN	WO200029584-A1.
PD	25-MAY-2000.
XX	
PF	16-NOV-1999; 99WC-US027153.
XX	
PR	18-NOV-1998; 98US-0108945P.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Chen YM, Lowman HB, Muller Y;
XX	
DR	WPI; 2000-387797/33.
XX	
XX	Antibody variants with higher binding affinity than native antibodies
PT	useful for diagnosis, prevention and treatment of neoplastic and non-
PT	neoplastic diseases comprises amino acid insertion in hypervariable
XX	region.
XX	
PS	Disclosure; Fig 1A; 110p; English.
XX	
CC	The present sequence is the light chain variable domain of F(ab)-12, a
CC	humanised anti-vascular endothelial growth factor (VEGF) antibody. F(ab)-
CC	12 was the parent antibody used in the production of a large number of
CC	antibody variants containing randomised peptide inserts within the
CC	complementarily determining regions (CDRs). Phage display libraries were
CC	subjected to eight rounds of selection to isolate variants with an
CC	antigen binding affinity at least two-fold stronger than the binding

CC affinity of parent antibody for the target VEGF antibody. The anti-VEGF
 CC antibody variants may be useful in diagnostic assays for detecting
 CC expression of VEGF in cells, tissue or serum. They may also be used in
 CC the prevention and treatment of neoplastic diseases such as breast
 CC cancer, lung cancer and retinoblastoma, and non-neoplastic diseases
 CC including rheumatoid arthritis, psoriasis, atherosclerosis, and diabetic
 CC and other proliferative retinopathies

XX Sequence 110 AA:

Query Match 100.0%; Score 576; DB 3; Length 110;
 Best Local Similarity 100.0%; Pred. No. 7.5e-33;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQKPKAPKVLIVFTSSLSHGVPS 60
 DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQKPKAPKVLIVFTSSLSHGVPS 60
 QY 61 RFSGSGSGTDFTLTISLSLOPEDPATYCCQYSTVPMFTFGGTVEIKRTV 110
 DB 61 RFSGSGSGTDFTLTISLSLOPEDPATYCCQYSTVPMFTFGGTVEIKRTV 110

RESULT 2

AA13376 standard; protein; 110 AA.

AA13376;

12-SEP-2003 (revised)
 21-NOV-2000 (first entry)

F(ab)-12 anti-VEGF antibody light chain variable domain.

Humanised; F(ab)-12; vascular endothelial cell growth factor; VEGF;
 antibody; antiinflammatory; cerebroprotective; cyostatic; antirheumatic;
 antiarthritic; antipsoriatic; antiarteriosclerotic; antidiabetic;
 antihypertoid; excessive neovascularisation; tumour; rheumatoid arthritis;
 psoriasis; atherosclerosis; diabetes; retrolental fibroplasia;
 neovascular glaucoma; haemangioma; thyroid hyperplasia; Grave's disease;
 tissue transplantation; inflammation; oedema; trauma;
 complementarity determining region; CDR.

OS Homo sapiens.

OS Mus sp.
 OS Chimeric.

Key Location/Qualifiers

Region 24..34 /label= CDR-L1

Region 50..56 /label= CDR-L2

Region 89..97 /label= CDR-L3

WO200037502-A2.

29-JUN-2000.

09-DEC-1999; 99WO-US029475.

22-DEC-1998; 98US-00218481.

(GETH) GENENTECH INC.

Van Bruggen N, Ferrara N;

WPI; 2000-442646/38.

Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis,
 diabetes and chronic inflammation in a mammal, comprises administering a
 human vascular endothelial cell growth factor antagonist.

PS Disclosure; Fig 1A; 60pp; English.

XX The present sequence is the light chain variable domain of humanised anti-
 CC -vascular endothelial cell growth factor (anti-VEGF) antibody F(ab)-12.
 CC It may be used to treat conditions characterised by undesirable excessive
 CC neovascularisation. Such conditions include tumours (especially solid
 CC ones), rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and
 CC other retinopathies, retrolental fibroplasia, age-related macular
 CC degeneration, neovascular glaucoma, haemangioma, thyroid hyperplasia
 CC (including Grave's disease), corneal and other tissue transplantation,
 CC and chronic inflammation. Oedemas associated with tumours, strokes and
 CC head trauma, and ascites associated with malignancies, myel's syndrome,
 CC lung inflammation, nephrotic syndrome, pericardial effusion and pleural
 CC effusion, may also be treated. Affinity matured anti-VEGF antibodies are
 CC also used as therapeutic agents. Monoclonal antibodies are generated in
 CC hybridoma cells and those with affinity for VEGF are identified by 12-SEP-
 CC immunoprecipitation or by an in vitro binding assay. (Updated on 12-SEP-
 CC 2003 to standardise OS field)

XX Sequence 110 AA:

Query Match 100.0%; Score 576; DB 3; Length 110;
 Best Local Similarity 100.0%; Pred. No. 7.5e-33;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQKPKAPKVLIVFTSSLSHGVPS 60
 DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQKPKAPKVLIVFTSSLSHGVPS 60
 QY 61 RFSGSGSGTDFTLTISLSLOPEDPATYCCQYSTVPMFTFGGTVEIKRTV 110
 DB 61 RFSGSGSGTDFTLTISLSLOPEDPATYCCQYSTVPMFTFGGTVEIKRTV 110

RESULT 3

ADQ90721 standard; protein; 237 AA.

ADQ90721;

21-OCT-2004 (first entry)

Anti-VEGF antibody light chain protein SEQ ID NO:25.

antibody; antigen binding fragment; cell culture; variable domain;
 modified framework region; hypervariable region; cyostatic;
 antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
 tumour; inflammatory disorder; angiogenic disorder;
 immunological disorder; anti-VEGF antibody;
 anti vascular endothelial cell growth factor antibody; light chain.

OS Homo sapiens.

OS Synthetic.

WO2004065417-A2.

05-AUG-2004.

23-JAN-2004; 2004WO-US001844.

23-JAN-2003; 2003US-0442484P.

(GETH) GENENTECH INC.

Simmons L;

WPI; 2004-562149/54.

N-PSDB; ADQ90720.

Producing an antibody or antigen binding fragment in high yield in a cell
 culture, comprises expressing a variable domain with a modified framework
 region in a host cell.

factor - for treatment of tumours, retinal disease and other angiogenic states, also related nucleic acid, vectors and transformed cells.

Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and chronic inflammation in a mammal, comprises administering a human vascular endothelial cell growth factor antagonist.

Disclosure; Fig 14A; 60pp; English.

XX The present sequence represents a variable light domain of an affinity-matured anti-vascular endothelial growth factor (anti-VEGF) antibody variant. The sequence is used in the course of the invention to produce the humanised anti-VEGF antibody of the invention. The humanised antibodies are used to inhibit VEGF-induced angiogenesis, particularly for treating or preventing tumours (of any type) and retinal disorders (e.g. age-related macular degeneration or diabetic retinopathy). They can also be used to treat other conditions that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc

XX The present sequence is the light chain variable region of the affinity-matured anti-vascular endothelial cell growth factor (anti-VEGF) antibody Y0117. Humanised Fab-12 and affinity matured anti-VEGF antibodies may be used to treat conditions characterised by undesirable excessive neovascularisation. Such conditions include tumours (especially solid ones), rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and other retinopathies, retrolental fibroplasia, age-related macular degeneration, neovascular glaucoma, haemangiomas, thyroid hyperplasia (including Grave's disease), corneal and other tissue transplantation, and chronic inflammation. Oedemas associated with tumours, strokes and head trauma, and ascites associated with malignancies, melig's syndrome, lung inflammation, nephrotic syndrome, pericardial effusion and pleural effusion, may also be treated. Monoclonal antibodies are generated in hybridoma cells and those with affinity for VEGF are identified by immunoprecipitation or by an in vitro binding assay

Query Match 99.5%; Score 573; DB 2; Length 110;
Best Local Similarity 99.1%; Pred. No. 1.2e-32;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPSSLSASVGDRTITCSASODISNYLWYQOKPKAPKVLITYFTSSLSHGVS 60
Db 1 DIQWTSPSSLSASVGDRTITCSASODISNYLWYQOKPKAPKVLITYFTSSLSHGVS 60

Qy 61 RFSGSGSGTDFTLTITSSLOPEDFATYYCQGYSTVPMTFGGQTKVEIKRTV 110
Db 61 RFSGSGSGTDFTLTITSSLOPEDFATYYCQGYSTVPMTFGGQTKVEIKRTV 110

RESULT 6

AB13380 ID AAB13380 standard; protein; 110 AA.

XX AAB13380;

DT 21-NOV-2000 (first entry)

XX Anti-VEGF antibody Y0317 light chain variable domain.

XX Y0317; vascular endothelial cell growth factor; VEGF; antibody;
KM antiinflammatory; cerebroprotective; cytoprotective; antihemmatic;
KM antiarthritic; antipsoriatic; antiarteriosclerotic; antidiabetic;
KM antithyroid; excessive neovascularisation; tumour; rheumatoid arthritis;
KM psoriasis; atherosclerosis; diabetes; retrolental fibroplasia;
KM neovascular glaucoma; haemangioma; thyroid hyperplasia; Grave's disease;
KM tissue transplantation; inflammation; oedema; trauma;
KM complementarity determining region; CDR.

XX Unidentified.

XX Key Location/Qualifiers
FT Region 24..33 /label= CDR-L1
FT Region 50..56 /label= CDR-L2
FT Region 89..97 /label= CDR-L3

XX WO200037502-A2.

XX 29-JUN-2000.

XX 09-DEC-1999; 99WO-US029475.

XX 22-DEC-1998; 98US-00218481.

XX (GETH) GENENTECH INC.

XX Van Bruggen N, Ferrara N;

XX WPI; 2000-442646/38.

XX

Query Match 99.5%; Score 573; DB 3; Length 110;
Best Local Similarity 99.1%; Pred. No. 1.2e-32;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTSPSSLSASVGDRTITCSASODISNYLWYQOKPKAPKVLITYFTSSLSHGVS 60
Db 1 DIQWTSPSSLSASVGDRTITCSASODISNYLWYQOKPKAPKVLITYFTSSLSHGVS 60

Qy 61 RFSGSGSGTDFTLTITSSLOPEDFATYYCQGYSTVPMTFGGQTKVEIKRTV 110
Db 61 RFSGSGSGTDFTLTITSSLOPEDFATYYCQGYSTVPMTFGGQTKVEIKRTV 110

RESULT 7

ABP61256 ID ABP61256 standard; protein; 110 AA.

XX ABP61256;

DT 20-SEP-2002 (first entry)

XX Humanised anti-VEGF Y0317 antibody variable light domain.

XX Cytoprotective; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
KM vascular endothelial growth factor; angiogenesis inhibitor; tumour;
KM retinal disorder; intraocular neovascular disorder; Y0317; light chain;
KM variable domain.

XX Homo sapiens.
OS Mus sp.
OS Synthetic.

XX Key Location/Qualifiers
FT Domain 24..34 /label= CDR-L1
FT Domain 50..56 /label= CDR-L2
FT Domain 89..97 /label= CDR-L3

XX US2002032315-A1.

XX 14-MAR-2002.

XX 06-APR-1998; 98US-00056160.

XX 06-AUG-1997; 97US-0054856P.

XX (BACA/) BACA M.

XX

PA (WELLS) WELLS J A.
 PA (PRES) PRESTA L G.
 PA (LOWM) LOWMAN H B.
 PA (CHEN) CHEN Y M.
 PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
 DR WPI; 2002-517920/55.
 XX
 XX New humanized anti-VEGF (vascular endothelial growth factor) antibodies
 PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
 PT mammal, particularly for treating tumor or retinal disorders.
 XX
 XX Claim 27; Fig 10; 47pp; English.
 XX
 XX The present invention relates to humanised anti-VEGF (vascular
 CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
 CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
 CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
 CC particularly those having a tumour or a retinal disorder e.g. intracocular
 CC neovascular disorders. The present sequence is an exemplary light chain
 CC variable domain of the humanised anti-VEGF antibody of the invention
 XX
 XX Sequence 110 AA;
 SQ

Query Match 99.5%; Score 573; DB 5; Length 110;
 Best Local Similarity 99.1%; Pred. No. 1.2e-32;
 Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTITCSASQDISNYLWYQOKPGKPKVLIYFTSSLHSGVPS 60
 DB 1 DIQMTSPSSLSASVGDRTITCSASQDISNYLWYQOKPGKPKVLIYFTSSLHSGVPS 60
 QY 61 RFSSGSGSTDFLTITSSLPEDPATYCCQYSTVPWTFGGTKVEIKRTV 110
 DB 61 RFSSGSGSTDFLTITSSLPEDPATYCCQYSTVPWTFGGTKVEIKRTV 110

RESULT 8
 ABP61246
 ID ABP61246 standard; protein; 110 AA.
 XX
 XX ABP61246;
 AC
 XX
 XX 20-SEP-2002 (first entry)
 DT
 XX
 XX Humanised anti-VEGF Y0101 antibody variable light domain.
 DB
 XX
 XX Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
 KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
 KW retinal disorder; intracocular neovascular disorder; Y0101; light chain;
 KW variable domain.
 XX
 XX Homo sapiens.
 OS Mus sp.
 OS Synthetic.
 OS
 XX
 XX Key Location/Qualifiers
 FT 24..34
 FT /label= CDR-L1
 FT 50..57
 FT /label= CDR-L2
 FT 89..97
 FT /label= CDR-L3
 XX
 XX US2002032315-A1.
 XX
 XX 14-MAR-2002.
 XX
 XX 06-APR-1998; 98US-00056160.
 XX
 XX 06-AUG-1997; 97US-0054856P.
 XX
 XX

PA (BACA) BACA M.
 PA (WELLS) WELLS J A.
 PA (PRES) PRESTA L G.
 PA (LOWM) LOWMAN H B.
 PA (CHEN) CHEN Y M.
 PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
 DR WPI; 2002-517920/55.
 XX
 XX New humanized anti-VEGF (vascular endothelial growth factor) antibodies
 PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
 PT mammal, particularly for treating tumor or retinal disorders.
 XX
 XX Example 3; Fig 9; 47pp; English.
 XX
 XX The present invention relates to humanised anti-VEGF (vascular
 CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
 CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
 CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
 CC particularly those having a tumour or a retinal disorder e.g. intracocular
 CC neovascular disorders. The present sequence is an exemplary light chain
 CC variable domain of the humanised anti-VEGF antibody of the invention
 XX
 XX Sequence 110 AA;
 SQ

Query Match 99.5%; Score 573; DB 5; Length 110;
 Best Local Similarity 99.1%; Pred. No. 1.2e-32;
 Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTITCSASQDISNYLWYQOKPGKPKVLIYFTSSLHSGVPS 60
 DB 1 DIQMTSPSSLSASVGDRTITCSASQDISNYLWYQOKPGKPKVLIYFTSSLHSGVPS 60
 QY 61 RFSSGSGSTDFLTITSSLPEDPATYCCQYSTVPWTFGGTKVEIKRTV 110
 DB 61 RFSSGSGSTDFLTITSSLPEDPATYCCQYSTVPWTFGGTKVEIKRTV 110

RESULT 9
 ADC26154
 ID ADC26154 standard; protein; 214 AA.
 XX
 XX ADC26154;
 AC
 XX
 XX 18-DEC-2003 (first entry)
 DT
 XX
 XX Parent anti-VEGF Y0101 antibody wild-type light chain protein.
 DE
 XX
 XX antibody variant; cytostatic; cancer; parent; anti-VEGF;
 KW vascular endothelial growth factor; Y0101; light chain; wild-type.
 KW
 XX
 XX Unidentified.
 OS
 OS
 OS WO2003068801-A2.
 OS
 OS
 OS 21-AUG-2003.
 OS
 OS 11-FEB-2003; 2003WO-US004184.
 OS
 OS 11-FEB-2002; 2002US-0355895P.
 OS 10-SEP-2002; 2002US-0409665P.
 OS
 OS (GETH) GENENTECH INC.
 OS
 OS Lowman HB, Marvin JS;
 OS
 OS WPI; 2003-697521/66.
 OS
 OS Making an antibody variant of a parent antibody specific to an antigen by
 PT identifying a target amino acid residue within the variable domain of the
 PT parent antibody and substituting the target residue with a different
 PT amino acid residue.
 PT

PT Novel Escherichia coli strain useful for producing polypeptide, deficient
PT in deep and ptc encoding protease, and harboring mutant spr gene, product
PT of gene suppresses growth phenotypes of strains harboring ptc mutants.
XX

PS Example 1, Fig 1A-C, 63pp, English.

CC The present invention describes an Escherichia coli strain (1) deficient
CC in chromosomal deep and ptc encoding protease deep and ptc, respectively,
CC and harbouring a mutant spr gene, the product of mutant spr gene
CC suppresses growth phenotypes exhibited by strains harbouring ptc mutants.
CC (1) is useful for producing a polypeptide, by culturing (1) comprising
CC nucleic acid encoding the polypeptide, which is heterologous to the
CC strain, such that the nucleic acid is expressed, and recovering the
CC heterologous polypeptide from the strain. The heterologous polypeptide is
CC proteolytically sensitive. Culturing of (1) is performed in a fermentor
CC under conditions of high- or low-cell density fermentation. The
CC polypeptide is recovered from the periplasm or culture medium of the
CC strain. The polypeptide is an antibody (humanised or full-length
CC antibody) or Apol2 ligand. The antibody is an anti-CD18, anti-vascular
CC endothelial growth factor (VEGF), anti-tissue factor, 2c4, anti-Her-2,
CC anti-CD20, anti-CD40, or anti-CD11a antibody. The antibody is also an
CC antibody fragment having a light chain (kappa light chain). The antibody
CC fragment is a Fab, Fab', Fab'2 or Fab'2-leucine zipper fusion, anti-CD18
CC Fab'2-leucine zipper fusion, anti-tissue factor Fab'2-leucine zipper
CC fusion or anti-VEGF Fab, with or without a histidine or lysine tag, anti-
CC tissue factor Fab'2-leucine zipper fusion with a 6-histidine tag, or anti-
CC Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-CD18
CC represents an anti-VEGF Fab amino acid sequence from the present
CC invention
XX

Sequence 237 AA:

Query Match 99.5%; Score 573; DB 5; Length 237;
Best Local Similarity 99.1%; Pred. No. 2.4e-32;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTQSSLSASVGRVITTCASQDISNYLMWYQKRGKAPKVIYFTSSLHSGVPS 60
Db 24 DIQWTQSSLSASVGRVITTCASQDISNYLMWYQKRGKAPKVIYFTSSLHSGVPS 83

QY 61 RFSGSGSGTDFTLTITSLQPEDFATYYCQQYSTVPMWFGQGTKEIKRTV 110
Db 84 RFSGSGSGTDFTLTITSLQPEDFATYYCQQYSTVPMWFGQGTKEIKRTV 133

RESULT 12
AD014128 standard; protein; 237 AA.

AD014128;

12-AUG-2004 (first entry)

Plasmid pXVG2AP11 expression cassette light chain protein SEQ ID NO:8.

antibody; variant heavy chain hinge region; immunoglobulin; cytoskeletal;
immunosuppressive; immunotherapy; tumour; cancer; immune disorder;
expression cassette; plasmid pXVG2AP11; anti-VEGF light chain.

Synthetic.

WO2004042017-A2.

21-MAY-2004.

30-OCT-2003; 2003WO-US034610.

31-OCT-2002; 2002US-0422952P.

(GETH) GENENTECH INC.

Relly D, Yansura DG;

XX WPI: 2004-390607/36.
DR N-PSDB; AD014127.

PT New antibody comprising a variant heavy chain hinge region incapable of
PT inter-heavy chain disulfide linkage, useful for treating, preventing,
PT diagnosing, delaying or preventing a disease, e.g. tumor, cancer or
PT immune disorder.

PS Example 1, SEQ ID NO 8; 124pp; English.

CC The present invention describes an antibody comprising a variant heavy
CC chain hinge region incapable of inter-heavy chain disulfide linkage. Also
CC described: (1) an antibody lacking inter-heavy chain disulfide linkage;
CC (2) an immunoglobulin comprising the antibody conjugated with a
CC heterologous moiety; (3) a composition comprising the antibody or
CC immunoglobulin, and carrier; (4) an article of manufacture comprising
CC the composition in a container; (5) a polynucleotide encoding the
CC antibody or immunoglobulin, or a variant immunoglobulin heavy chain
CC incapable of inter-heavy chain disulfide linkage; (6) a recombinant
CC vector for expressing the antibody or immunoglobulin; (7) a host cell
CC comprising the recombinant vector; (8) expressing in a host cell an
CC antibody of interest in which at least one inter-heavy chain disulfide
CC linkage is eliminated, and recovering the antibody from the host cell;
CC (9) an aglycosylated antibody produced by the method; and (10) treating,
CC preventing, diagnosing, delaying or preventing a disease in a subject.
CC The antibody has cytoskeletal and immunosuppressive activities, and can be
CC used in immunotherapy. The antibody, immunoglobulin and methods are
CC useful for treating, preventing, diagnosing, delaying or preventing a
CC disease, e.g. tumor, cancer or immune disorder. The present sequence
CC represents the anti-VEGF light chain from the expression cassette of
CC plasmid pXVG2AP11, which is used in the exemplification of the present
CC invention.
XX

Sequence 237 AA:

Query Match 99.5%; Score 573; DB 8; Length 237;
Best Local Similarity 99.1%; Pred. No. 2.4e-32;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTQSSLSASVGRVITTCASQDISNYLMWYQKRGKAPKVIYFTSSLHSGVPS 60
Db 24 DIQWTQSSLSASVGRVITTCASQDISNYLMWYQKRGKAPKVIYFTSSLHSGVPS 83

QY 61 RFSGSGSGTDFTLTITSLQPEDFATYYCQQYSTVPMWFGQGTKEIKRTV 110
Db 84 RFSGSGSGTDFTLTITSLQPEDFATYYCQQYSTVPMWFGQGTKEIKRTV 133

RESULT 13
AD014131 standard; protein; 237 AA.

AD014131;

12-AUG-2004 (first entry)

Plasmid pXVG11NERK expression cassette light chain protein SEQ ID NO:11.

antibody; variant heavy chain hinge region; immunoglobulin; cytoskeletal;
immunosuppressive; immunotherapy; tumour; cancer; immune disorder;
expression cassette; plasmid pXVG11NERK; anti-VEGF light chain.

Synthetic.

WO2004042017-A2.

21-MAY-2004.

30-OCT-2003; 2003WO-US034610.

31-OCT-2002; 2002US-0422952P.

PA (GERTH) GENENTECH INC.
 XX
 PI Relilly D, Yamsura DG;
 XX
 DR WPI; 2004-390607/36.
 DR N-PSDB; ADO14130.
 XX
 PT New antibody comprising a variant heavy chain hinge region incapable of
 PT inter-heavy chain disulfide linkage, useful for treating, preventing,
 PT diagnosing, delaying or preventing a disease, e.g. tumor, cancer or
 PT immune disorder.
 XX
 PS Example 1; SEQ ID NO 11; 124pp; English.
 XX
 CC The present invention describes an antibody comprising a variant heavy
 CC chain hinge region incapable of inter-heavy chain disulfide linkage. Also
 CC described: (1) an antibody lacking inter-heavy chain disulfide linkage;
 CC (2) an immunocjugate comprising the antibody conjugated with a
 CC heterologous moiety; (3) a composition comprising the antibody or
 CC immunocjugate, and carrier; (4) an article of manufacture comprising
 CC the composition in a container; (5) a polynucleotide encoding the
 CC antibody or immunocjugate, or a variant immunoglobulin heavy chain
 CC incapable of inter-heavy chain disulfide linkage; (6) a recombinant
 CC vector for expressing the antibody or immunocjugate; (7) a host cell
 CC comprising the recombinant vector; (8) expressing in a host cell an
 CC antibody of interest in which at least one inter-heavy chain disulfide
 CC linkage is eliminated, and recovering the antibody from the host cell;
 CC (9) an glycosylated antibody produced by the method; and (10) treating,
 CC preventing, diagnosing, delaying or preventing a disease in a subject.
 CC The antibody has cytostatic and immunosuppressive activities, and can be
 CC used in immunotherapy. The antibody, immunocjugate and methods are
 CC useful for treating, preventing, diagnosing, delaying or preventing a
 CC disease, e.g. tumor, cancer or immune disorder. The present sequence
 CC represents the anti-VEGF light chain from the expression cassette of
 CC plasmid pXVG11VERK, which is used in the exemplification of the present
 CC invention.
 CC
 XX
 SQ Sequence 237 AA;
 Query Match 99.5%; Score 573; DB 8; Length 237;
 Best Local Similarity 99.1%; Pred. No. 2,4e-32;
 Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQWTGSPSSLSASVGBRVITTCASQDISNYLNMWYQKPKAPKVLITFTSSLSHSGVPS 60
 DB 24 DIQWTGSPSSLSASVGBRVITTCASQDISNYLNMWYQKPKAPKVLITFTSSLSHSGVPS 83
 QY 61 RFGSGSGGTDFLTITISLQPEDPATYTCQOYSTVPMWFGGCTVVEIKRTV 110
 DB 84 RFGSGSGGTDFLTITISLQPEDPATYTCQOYSTVPMWFGGCTVVEIKRTV 133
 RESULT 14
 ADO90703
 XX ADO90703 standard; protein; 237 AA.
 AC ADO90703;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Anti-VEGF antibody Y0317 light chain protein SEQ ID NO:7.
 XX
 KW antibody; antigen binding fragment; cell culture; variable domain;
 KW modified framework region; hypervariable region; cytosolic;
 KW antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
 KW tumour; inflammatory disorder; angiogenic disorder;
 KW immunological disorder; anti-VEGF antibody;
 KW anti vascular endothelial cell growth factor antibody; light chain.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO2004065417-A2.

XX
 PD 05-AUG-2004.
 XX
 XX 23-JAN-2004; 2004MO-US001844.
 PE
 XX 23-JAN-2003; 2003US-0442484P.
 PR
 XX
 PA (GERTH) GENENTECH INC.
 XX
 PI Simmons L;
 XX
 DR WPI; 2004-562149/54.
 DR N-PSDB; ADO90702.
 XX
 PT Producing an antibody or antigen binding fragment in high yield in a cell
 PT culture, comprises expressing a variable domain with a modified framework
 PT region in a host cell.
 XX
 PS Example 2; SEQ ID NO 7; 161pp; English.
 XX
 CC The present invention describes a method for producing an antibody or
 CC antigen binding fragment in high yield in a cell culture. The method
 CC comprises expressing a variable domain of the antibody or antigen binding
 CC fragment comprising a modified framework region (FR) in a host cell, and
 CC recovering the antibody or antigen binding fragment variable domain
 CC comprising the modified framework from the host cell. The modified FR in
 CC the method described above has a substitution of at least one amino acid
 CC position with a different amino acid, where the different amino acid is
 CC the amino acid found at the corresponding FR position of a human subgroup
 CC variable domain consensus sequence that has a hypervariable region 1
 CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
 CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
 CC The antibody or antigen binding fragment variable domain comprises the
 CC modified FR that has improved yield in cell culture compared to an
 CC unmodified antibody or antigen-binding fragment. The antibody and antigen
 CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and
 CC immunomodulatory activities, and can be used in antibody therapy. The
 CC methods and compositions of the present invention are useful for
 CC producing antibodies or antigen binding fragments in cell culture, in
 CC particular for improving the yield of recombinant antibodies or antigen
 CC binding fragments in cell culture. The antibodies of the invention can be
 CC used to diagnose, treat, inhibit or prevent e.g. tumours and
 CC inflammatory, angiogenic and immunological disorders. The present
 CC sequence represents the light chain of an anti-VEGF (vascular endothelial
 CC cell growth factor) antibody, which is used in the exemplification of the
 CC present invention.
 CC
 XX
 SQ Sequence 237 AA;
 Query Match 99.5%; Score 573; DB 8; Length 237;
 Best Local Similarity 99.1%; Pred. No. 2,4e-32;
 Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQWTGSPSSLSASVGBRVITTCASQDISNYLNMWYQKPKAPKVLITFTSSLSHSGVPS 60
 DB 24 DIQWTGSPSSLSASVGBRVITTCASQDISNYLNMWYQKPKAPKVLITFTSSLSHSGVPS 83
 QY 61 RFGSGSGGTDFLTITISLQPEDPATYTCQOYSTVPMWFGGCTVVEIKRTV 110
 DB 84 RFGSGSGGTDFLTITISLQPEDPATYTCQOYSTVPMWFGGCTVVEIKRTV 133
 RESULT 15
 ADO90701
 XX ADO90701 standard; protein; 237 AA.
 AC ADO90701;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Anti-VEGF antibody VNERK light chain protein SEQ ID NO:5.
 DE
 XX antibody; antigen binding fragment; cell culture; variable domain;
 KW

Job time : 89.0482 secs

KW modified framework region; hypervariable region; cytosolic;
 KW antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
 KW tumour; inflammatory disorder; angiogenic disorder;
 KW immunological disorder; anti-VEGF antibody;
 KW anti vascular endothelial cell growth factor antibody; light chain.

OS Homo sapiens.
 OS Synthetic.

PN WO2004065417-A2.

PD 05-AUG-2004.

PF 23-JAN-2004; 2004WO-US001844.

PR 23-JAN-2003; 2003US-0442484P.

PA (GETH) GENENTECH INC.

PI Simmons L;

DR WPI; 2004-562149/54.

DR N-PSDB; ADQ90700.

PT Producing an antibody or antigen binding fragment in high yield in a cell
 PT culture, comprises expressing a variable domain with a modified framework
 PT region in a host cell.

PS Example 2; SEQ ID NO 5; 161pp; English.

CC The present invention describes a method for producing an antibody or
 CC antigen binding fragment in high yield in a cell culture. The method
 CC comprises expressing a variable domain of the antibody or antigen binding
 CC fragment comprising a modified framework region (FR) in a host cell, and
 CC recovering the antibody or antigen binding fragment variable domain
 CC comprising the modified framework from the host cell. The modified FR in
 CC the method described above has a substitution of at least one amino acid
 CC position with a different amino acid, where the different amino acid is
 CC the amino acid found at the corresponding FR position of a human subgroup
 CC variable domain consensus sequence that has a hypervariable region 1
 CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
 CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
 CC The antibody or antigen binding fragment variable domain comprises the
 CC modified FR that has improved yield in cell culture compared to an
 CC unmodified antibody or antigen-binding fragment. The antibody and antigen
 CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and
 CC immunomodulatory activities, and can be used in antibody therapy. The
 CC methods and compositions of the present invention are useful for
 CC producing antibodies or antigen binding fragments in cell culture, in
 CC particular for improving the yield of recombinant antibodies or antigen
 CC binding fragments in cell culture. The antibodies of the invention can be
 CC used to diagnose, treat, inhibit or prevent e.g. tumours and
 CC inflammatory, angiogenic and immunological disorders. The present
 CC sequence represents the light chain of an anti-VEGF (vascular endothelial
 CC cell growth factor) antibody, which is used in the exemplification of the
 CC present invention.

CC Sequence 237 AA;

QY Query Match 99.5%; Score 573; DB 8; Length 237;
 Db Best Local Similarity 99.1%; Pred. No. 2.4e-32;
 Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGRPTTTCASODISNTLNTYQOKRGAAPKLYITFTSSLSHGVPVS 60
 Db 24 DIQMTSPSSLSASVGRPTTTCASODISNTLNTYQOKRGAAPKLYITFTSSLSHGVPVS 83

QY 61 RPSGSGSGTDFLTITSSLOPEDFATYCCQYSTVPWTFGQGTKEIKRTV 110
 Db 84 RPSGSGSGTDFLTITSSLOPEDFATYCCQYSTVPWTFGQGTKEIKRTV 133

Search completed: March 14, 2005, 20:39:16

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2005, 20:30:13 ; Search time 22.6754 Seconds
(without alignments)
362.127 Million cell updates/sec

Title: US-09-723-752b-8

Perfect score: 576
Sequence: 1 DIQMTSPSSLSASVGDRTV.....YSTVPTFGGTVKEIKRTV 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/prodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/prodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/prodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/prodata/1/1aa/PCUS.COMB.pep.*
6: /cgn2_6/prodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	576	100.0	110 4 US-09-440-781-94	Sequence 94, Appl
2	567	98.4	491 4 US-10-011-125A-2	Sequence 2, Appl
3	554	96.2	110 4 US-09-440-781-95	Sequence 95, Appl
4	525	91.1	214 2 US-07-934-373C-40	Sequence 40, Appl
5	525	91.1	214 2 US-08-788-800-11	Sequence 11, Appl
6	525	91.1	214 3 US-08-437-642B-40	Sequence 40, Appl
7	525	91.1	214 3 US-09-097-309-2	Sequence 2, Appl
8	525	91.1	214 3 US-09-097-171A-2	Sequence 2, Appl
9	525	91.1	214 3 US-09-460-587-2	Sequence 2, Appl
10	525	91.1	214 4 US-09-940-166A-2	Sequence 2, Appl
11	525	91.1	214 5 PCT-US93-07832-40	Sequence 40, Appl
12	525	91.1	233 3 US-07-934-373C-25	Sequence 25, Appl
13	525	91.1	233 3 US-08-437-642B-25	Sequence 25, Appl
14	525	91.1	233 4 US-08-146-206C-25	Sequence 25, Appl
15	525	91.1	233 4 US-09-705-686-25	Sequence 25, Appl
16	525	91.1	233 4 US-09-705-392A-25	Sequence 25, Appl
17	525	91.1	233 4 US-09-705-398-25	Sequence 25, Appl
18	525	91.1	233 5 PCT-US93-07832-25	Sequence 25, Appl
19	525	91.1	237 3 US-09-097-309-6	Sequence 6, Appl
20	525	91.1	237 3 US-09-097-171A-10	Sequence 10, Appl
21	525	91.1	237 3 US-09-432-712B-2	Sequence 2, Appl
22	525	91.1	237 3 US-09-607-756-2	Sequence 2, Appl
23	525	91.1	237 3 US-09-460-587-6	Sequence 6, Appl
24	525	91.1	237 4 US-09-940-166A-6	Sequence 6, Appl
25	525	90.6	214 1 US-08-458-516A-12	Sequence 12, Appl
26	521	90.5	109 2 US-07-934-373C-47	Sequence 47, Appl
27	521	90.5	109 3 US-08-437-642B-47	Sequence 47, Appl

28	517	89.8	214 2 US-07-934-373C-39	Sequence 39, Appl
29	517	89.8	214 3 US-08-437-642B-39	Sequence 39, Appl
30	517	89.8	214 5 PCT-US93-07832-39	Sequence 39, Appl
31	514	89.2	107 2 US-07-934-373C-17	Sequence 17, Appl
32	514	89.2	107 3 US-08-437-642B-17	Sequence 17, Appl
33	514	89.2	107 4 US-08-146-206C-17	Sequence 17, Appl
34	514	89.2	107 4 US-09-705-686-17	Sequence 17, Appl
35	514	89.2	107 4 US-09-705-392A-17	Sequence 17, Appl
36	514	89.2	107 4 US-09-705-398-17	Sequence 17, Appl
37	514	89.2	107 5 PCT-US93-07832-17	Sequence 17, Appl
38	514	89.2	108 3 US-08-974-899-3	Sequence 3, Appl
39	514	89.2	108 4 US-09-795-798-3	Sequence 3, Appl
40	514	89.2	127 3 US-08-649-100-33	Sequence 33, Appl
41	510	88.5	109 2 US-07-934-373C-3	Sequence 3, Appl
42	510	88.5	109 3 US-08-437-642B-3	Sequence 3, Appl
43	510	88.5	109 4 US-08-146-206C-3	Sequence 3, Appl
44	510	88.5	109 4 US-09-705-686-3	Sequence 3, Appl
45	510	88.5	109 4 US-09-705-392A-3	Sequence 3, Appl

ALIGNMENTS

```

RESULT 1
US-09-440-781-94
Sequence 94, Application US/09440781
Patent No. 6632926
GENERAL INFORMATION:
APPLICANT: Yvonne Man-yea Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 94
LENGTH: 110
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-110
OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-94

Query Match      100.0%; Score 576; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 2.8e-47;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DIQMTSPSSLSASVGDRTVITCSAODISNINMYOQKPKAKVLIYFTSSLHSGVPS 60
DB      1 DIQMTSPSSLSASVGDRTVITCSAODISNINMYOQKPKAKVLIYFTSSLHSGVPS 60
QY      61 RFSGSSGSDFTLTISLQPEDFATYCCOYSTVPTFGGTVKEIKRTV 110
DB      61 RFSGSSGSDFTLTISLQPEDFATYCCOYSTVPTFGGTVKEIKRTV 110

RESULT 2
US-10-011-125A-2
Sequence 2, Application US/1001125A
Patent No. 6828121
GENERAL INFORMATION:
APPLICANT: Chen, Christina Yu-Ching
TITLE OF INVENTION: BACTERIAL HOST STRAINS
FILE REFERENCE: P1804R1
CURRENT APPLICATION NUMBER: US/10/011,125A
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 2
LENGTH: 491
TYPE: PRT

```

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sequence is synthesized.
Patent No. 6828121
US-10-011-125A-2

Query Match 98.4%; Score 567; DB 4; Length 491;
Best Local Similarity 97.3%; Pred. No. 1.1e-45;
Matches 107; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGRVTITCSASODISNYLWYQKPKKLYIFTSSLSHGVPS 60
DB 24 DIQMTSPSSLSASVGRVTITCSASODISNYLWYQKPKKLYIFTSSLSHGVPS 83
QY 61 RFGSGSGDTFTLTITSSLOPEDFATYCCQYSTVPMFGGTKEIKRTV 110
DB 84 RFGSGSGDTFTLTITSSLOPEDFATYCCQYSTVPMFGGTKEIKRTV 123

RESULT 3
US-09-440-781-95
Sequence 95; Application US/09440781
Patent No. 6613926
GENERAL INFORMATION:
APPLICANT: Yvonne Man-yea Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 95
LENGTH: 110
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-110
OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-95

Query Match 96.2%; Score 554; DB 4; Length 110;
Best Local Similarity 94.5%; Pred. No. 3.4e-45;
Matches 104; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGRVTITCSASODISNYLWYQKPKKLYIFTSSLSHGVPS 60
DB 1 DIQMTSPSSLSASVGRVTITCSASODISNYLWYQKPKKLYIFTSSLSHGVPS 60
QY 61 RFGSGSGDTFTLTITSSLOPEDFATYCCQYSTVPMFGGTKEIKRTV 110
DB 61 RFGSGSGDTFTLTITSSLOPEDFATYCCQYSTVPMFGGTKEIKRTV 110

RESULT 4
US-07-934-373C-40
Sequence 40; Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-40

Query Match 91.1%; Score 525; DB 2; Length 214;
Best Local Similarity 90.9%; Pred. No. 3.9e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGRVTITCSASODISNYLWYQKPKKLYIFTSSLSHGVPS 60
DB 1 DIQMTSPSSLSASVGRVTITCSASODISNYLWYQKPKKLYIFTSSLSHGVPS 60
QY 61 RFGSGSGDTFTLTITSSLOPEDFATYCCQYSTVPMFGGTKEIKRTV 110
DB 61 RFGSGSGDTFTLTITSSLOPEDFATYCCQYSTVPMFGGTKEIKRTV 110

RESULT 5
US-08-788-800-11
Sequence 11; Application US/08788800
Patent No. 5914112
GENERAL INFORMATION:
APPLICANT: Bednar, Martin M.
APPLICANT: Thomas, G. Roger
APPLICANT: Gross, Cordell E.
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,800
FILING DATE: 22-Jan-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0987r1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-788-800-11

Query Match 91.1%; Score 525; DB 2; Length 214;
Best Local Similarity 90.9%; Pred. No. 3.9e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTTTCASQDISNTYLMWYQKPKAPKVLITFTSLHSGVPS 60
DB 1 DIOMTQSPSSLSASVGDRTTTCASQDISNTYLMWYQKPKAPKVLITFTSLHSGVPS 60
QY 61 RFSGSGSGTDYTLTITSLQPEDPATYTCQOQNTLPPTFGQGTKEIKRTV 110
DB 61 RFSGSGSGTDYTLTITSLQPEDPATYTCQOQNTLPPTFGQGTKEIKRTV 110

RESULT 6

US-08-437-642B-40
Sequence 40, Application US/08437642B
Patent No. 6054237

GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-437-642B-40

Query Match 91.1%; Score 525; DB 3; Length 214;
Best Local Similarity 90.9%; Pred. No. 3.9e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTTTCASQDISNTYLMWYQKPKAPKVLITFTSLHSGVPS 60
DB 1 DIOMTQSPSSLSASVGDRTTTCASQDISNTYLMWYQKPKAPKVLITFTSLHSGVPS 60
QY 61 RFSGSGSGTDYTLTITSLQPEDPATYTCQOQNTLPPTFGQGTKEIKRTV 110
DB 61 RFSGSGSGTDYTLTITSLQPEDPATYTCQOQNTLPPTFGQGTKEIKRTV 110

RESULT 7

US-09-097-309-2
Sequence 2, Application US/09097309
Patent No. 6121428

GENERAL INFORMATION:
APPLICANT: Blank, Gregory S.
APPLICANT: Narindray, Daljit S.
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: Protein Recovery
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,309
FILING DATE: 12-Jun-1998

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050951
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-7467
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-09-097-309-2

Query Match 91.1%; Score 525; DB 3; Length 214;
Best Local Similarity 90.9%; Pred. No. 3.9e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTTTCASQDISNTYLMWYQKPKAPKVLITFTSLHSGVPS 60
DB 1 DIOMTQSPSSLSASVGDRTTTCASQDISNTYLMWYQKPKAPKVLITFTSLHSGVPS 60
QY 61 RFSGSGSGTDYTLTITSLQPEDPATYTCQOQNTLPPTFGQGTKEIKRTV 110
DB 61 RFSGSGSGTDYTLTITSLQPEDPATYTCQOQNTLPPTFGQGTKEIKRTV 110

RESULT 8

US-09-097-171A-2
Sequence 2, Application US/09097171A
Patent No. 6171586

GENERAL INFORMATION:
APPLICANT: Lam, Xanthe M.
APPLICANT: Oeswein, James Q.

APPLICANT: Ongridpatanakul, Boonari
APPLICANT: Shahrokh, Zahra
APPLICANT: Wang, Sharon X.
APPLICANT: Weisburg, Robert P.
APPLICANT: Wong, Rita L.
TITLE OF INVENTION: Antibody Formulation
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,171A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/874897
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1089R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/425-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-097-171A-2

Query Match 91.1%; Score 525; DB 3; Length 214;
Best Local Similarity 90.9%; Pred. No. 3.9e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDRTTITCSASODISNINLWYQOKPGKAPKLLIYFTSLHSGVGS 60
|||
DB 1 DIQMTQSPSSLSASVDRTTITCRASQDINNINLWYQOKPGKAPKLLIYFTSLHSGVGS 60
|||
QY 61 RFGSGSGTDFTLTISLSLOPEDPATYCCQYSTVPMWTFGGGTVEIKRTV 110
|||
DB 61 RFGSGSGTDYITLTISLSLOPEDPATYCCQAGNTLPTFGGTVEIKRTV 110
|||

RESULT 9
US-09-460-587-2
Sequence 2, Application US/09460587
Patent No. 6322997
GENERAL INFORMATION:
APPLICANT: Blank, Gregory S.
APPLICANT: Narindray, Daljit S.
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: Protein Recovery
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/460,587
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/097,309
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-7467
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-460-587-2

Query Match 91.1%; Score 525; DB 3; Length 214;
Best Local Similarity 90.9%; Pred. No. 3.9e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDRTTITCSASODISNINLWYQOKPGKAPKLLIYFTSLHSGVGS 60
|||
DB 1 DIQMTQSPSSLSASVDRTTITCRASQDINNINLWYQOKPGKAPKLLIYFTSLHSGVGS 60
|||
QY 61 RFGSGSGTDFTLTISLSLOPEDPATYCCQYSTVPMWTFGGGTVEIKRTV 110
|||
DB 61 RFGSGSGTDYITLTISLSLOPEDPATYCCQAGNTLPTFGGTVEIKRTV 110
|||

RESULT 10
US-09-940-166A-2
Sequence 2, Application US/09940166A
Patent No. 6716598
GENERAL INFORMATION:
APPLICANT: Blank, Gregory S.
APPLICANT: Narindray, Daljit S.
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: Protein Recovery
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/940,166A
FILING DATE: 27-AUG-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/097,309
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-7467
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2
US-09-940-166A-2

Query Match 91.1%; Score 525; DB 4; Length 214;
Best Local Similarity 90.9%; Pred. No. 3.9e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGDVVTITCSASQDISNYLNMWYQKPKAKPRLIYFTSLHSGVPS 60
DB 1 DIQWTQSPSSLSASVGDVVTITCSASQDISNYLNMWYQKPKAKPRLIYFTSLHSGVPS 60
DB 61 RFSGSGSGDTYTLTISLSLOPEDFATYYCOQGNLTPPTFGGTKEIKRTV 110
QY 61 RFSGSGSGDTYTLTISLSLOPEDFATYYCOQYSTVPMFTGGTKEIKRTV 110
DB 61 RFSGSGSGDTYTLTISLSLOPEDFATYYCOQGNLTPPTFGGTKEIKRTV 110

RESULT 11
PCT-US93-07832-40
Sequence 40, Application PC/TUS9307832
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Pointe San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 709P2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US93-07832-40

Query Match 91.1%; Score 525; DB 5; Length 214;
Best Local Similarity 90.9%; Pred. No. 3.9e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
QY 1 DIQWTQSPSSLSASVGDVVTITCSASQDISNYLNMWYQKPKAKPRLIYFTSLHSGVPS 60
DB 1 DIQWTQSPSSLSASVGDVVTITCSASQDISNYLNMWYQKPKAKPRLIYFTSLHSGVPS 60

DB 1 DIQWTQSPSSLSASVGDVVTITCSASQDISNYLNMWYQKPKAKPRLIYFTSLHSGVPS 60
QY 61 RFSGSGSGDTYTLTISLSLOPEDFATYYCOQYSTVPMFTGGTKEIKRTV 110
DB 61 RFSGSGSGDTYTLTISLSLOPEDFATYYCOQGNLTPPTFGGTKEIKRTV 110

RESULT 12
US-07-934-373C-25
Sequence 25, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-07-934-373C-25

Query Match 91.1%; Score 525; DB 2; Length 233;
Best Local Similarity 90.9%; Pred. No. 4.3e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGDVVTITCSASQDISNYLNMWYQKPKAKPRLIYFTSLHSGVPS 60
DB 20 DIQWTQSPSSLSASVGDVVTITCSASQDISNYLNMWYQKPKAKPRLIYFTSLHSGVPS 79
QY 61 RFSGSGSGDTYTLTISLSLOPEDFATYYCOQYSTVPMFTGGTKEIKRTV 110
DB 80 RFSGSGSGDTYTLTISLSLOPEDFATYYCOQGNLTPPTFGGTKEIKRTV 129

RESULT 13
US-08-437-642B-25
Sequence 25, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants

NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-25

Query Match 91.1%; Score 525; DB 3; Length 233;
Best Local Similarity 90.9%; Pred. No. 4,3e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIOMTSPSSLSASVGRVTTTCSASODISNYLNMWYQKRGKAPKVLITYTSSLSHGVPS 60
DB 20 DIOMTSPSSLSASVGRVTTTCSASODINNYLNMWYQKRGKAPKVLITYTSSLSHGVPS 79

QY 61 RFGSGSGDTFTLTITSSLOPEDFATYCCQYSTVPMTFGGTKVEIKRTV 110
DB 80 RFGSGSGDTFTLTITSSLOPEDFATYCCQGNLTLPFTGGTKVEIKRTV 129

RESULT 14
US-08-146-206C-25
Sequence 25, Application US/08146206C
Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-No. 6407213-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-146-206C-25

Query Match 91.1%; Score 525; DB 4; Length 233;
Best Local Similarity 90.9%; Pred. No. 4,3e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIOMTSPSSLSASVGRVTTTCSASODISNYLNMWYQKRGKAPKVLITYTSSLSHGVPS 60
DB 20 DIOMTSPSSLSASVGRVTTTCSASODINNYLNMWYQKRGKAPKVLITYTSSLSHGVPS 79

QY 61 RFGSGSGDTFTLTITSSLOPEDFATYCCQYSTVPMTFGGTKVEIKRTV 110
DB 80 RFGSGSGDTFTLTITSSLOPEDFATYCCQGNLTLPFTGGTKVEIKRTV 129

RESULT 15
US-09-705-686-25
Sequence 25, Application US/09705686
Patent No. 6639055
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-No. 6639055-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D3
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-705-686-25

Query Match 91.1%; Score 525; DB 4; Length 233;
Best Local Similarity 90.9%; Pred. No. 4.3e-42;
Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTYITCSASODISNINLNTYQKPKAPKVLITYFTSLHSGVPS 60
|||
Db 20 DIQMTQSPSSLSASVGDRTYITCRASODININLNTYQKPKAPKVLITYFTSLHSGVPS 79
|||
Qy 61 RPSGSGSGTDFLTITISLOPEDPATYCCOYSTVPMTPGQGTKEIKRTV 110
|||
Db 80 RPSGSGSGTDFLTITISLOPEDPATYCCOQNTLPPTFGQGTKEIKRTV 129
|||

Search completed: March 14, 2005, 20:43:52
Job time : 23.6754 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using BW model

Run on: March 14, 2005, 20:22:02 ; Search time 41.0088 Seconds
(without alignments)
884.760 Million cell updates/sec

Title: US-09-723-752b-8

Perfect score: 576
Sequence: 1 DIQWTGSPSSISASVGRVT.....YSTVPWTFGQGTKEIKRTV 110

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubppaa/PCR_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	576	100.0	110	14	US-10-234-671-8
2	576	100.0	110	15	US-10-624-153-94
3	573	99.5	110	9	US-09-056-1608-107
4	573	99.5	110	9	US-09-056-1608-117
5	573	99.5	110	14	US-10-234-671-105
6	573	99.5	110	14	US-10-234-671-115
7	573	99.5	213	16	US-10-379-392-135
8	573	99.5	213	16	US-10-379-392-137
9	573	99.5	213	15	US-10-379-392-139
10	573	99.5	214	15	US-10-364-953-1
11	573	99.5	237	14	US-10-020-786-10
12	573	99.5	237	17	US-10-697-995-8
13	573	99.5	237	17	US-10-697-995-11

14	570	99.0	110	9	US-09-056-1608-105	Sequence 105, App
15	570	99.0	110	14	US-10-234-671-103	Sequence 103, App
16	569	98.8	213	16	US-10-379-392-155	Sequence 155, App
17	568	98.6	213	16	US-10-379-392-153	Sequence 153, App
18	567	98.4	108	9	US-09-056-1608-8	Sequence 8, App1
19	567	98.4	108	13	US-10-153-159-2	Sequence 2, App1
20	567	98.4	108	13	US-10-153-159-16	Sequence 16, App1
21	567	98.4	108	14	US-10-153-176-2	Sequence 2, App1
22	567	98.4	108	14	US-10-153-176-16	Sequence 16, App1
23	567	98.4	108	15	US-10-443-134A-2	Sequence 2, App1
24	567	98.4	108	15	US-10-443-134A-16	Sequence 16, App1
25	567	98.4	108	17	US-10-443-134A-127	Sequence 127, App
26	567	98.4	108	17	US-10-877-532-7	Sequence 7, App1
27	567	98.4	110	9	US-09-056-1608-103	Sequence 103, App
28	567	98.4	110	14	US-10-234-671-101	Sequence 101, App
29	567	98.4	237	9	US-09-056-1608-100	Sequence 100, App
30	567	98.4	237	14	US-10-234-671-100	Sequence 100, App
31	567	98.4	491	13	US-10-011-125-2	Sequence 2, App1
32	565	98.1	213	16	US-10-379-392-157	Sequence 157, App
33	564	97.9	108	13	US-10-153-159-4	Sequence 4, App1
34	564	97.9	108	14	US-10-153-176-4	Sequence 4, App1
35	564	97.9	108	15	US-10-443-134A-4	Sequence 4, App1
36	562	97.6	107	16	US-10-723-434-1	Sequence 1, App1
37	561	97.4	108	9	US-09-056-1608-126	Sequence 126, App
38	561	97.4	108	14	US-10-234-671-124	Sequence 124, App
39	559	97.0	107	9	US-09-056-1608-13	Sequence 13, App1
40	559	97.0	107	14	US-10-234-671-13	Sequence 13, App1
41	556	96.5	107	9	US-09-056-1608-15	Sequence 15, App1
42	556	96.5	107	14	US-10-234-671-15	Sequence 15, App1
43	556	96.5	214	15	US-10-364-953-4	Sequence 4, App1
44	555	96.4	214	15	US-10-364-953-3	Sequence 3, App1
45	554	96.2	110	9	US-09-056-1608-109	Sequence 109, App

ALIGNMENTS

RESULT 1

US-10-234-671-8
Sequence 8, Application US/10234671
Publication No. US20030190317A1

GENERAL INFORMATION:

APPLICANT: Baca, Manuel

Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.

TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way

CITY: South San Francisco
STATE: California

COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234, 671

FILING DATE: 03-Sep-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160

FILING DATE: 06-APR-1998

APPLICATION NUMBER: 60/126446

FILING DATE: 07-APR-1997

APPLICATION NUMBER: 60/054856

FILING DATE: 06-AUG-1997

ATTORNEY/AGENT INFORMATION:

NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-10-234-671-8
SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Query Match 100.0%; Score 576; DB 14; Length 110;
Best Local Similarity 100.0%; Pred. No. 8.4e-41;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTVITCSASODISNYLNMWQOKPKAPKVLITYFTSSLSHSGVPS 60
DB 1 DIQMTSPSSLSASVGDRTVITCSASODISNYLNMWQOKPKAPKVLITYFTSSLSHSGVPS 60

QY 61 RFGSGSGTDFTLTITSSLOPEDPATYCCOQYSTVPMTFGGGTVEIKRTV 110
DB 61 RFGSGSGTDFTLTITSSLOPEDPATYCCOQYSTVPMTFGGGTVEIKRTV 110

RESULT 2
US-10-624-153-94
Sequence 94, Application US/10624153
Publication No. US20040086502A1
GENERAL INFORMATION:
APPLICANT: CHEN, YVONNE M.
APPLICANT: LOWMAN, HENRY B.
APPLICANT: MULLER, YVES
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1C1
CURRENT APPLICATION NUMBER: US/10/624,153
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: US 09/440,781
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: US 60/108,945
PRIOR FILING DATE: 1998-11-18
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 94
LENGTH: 110
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
NAME/KEY: artificial
LOCATION: 1-110
OTHER INFORMATION: humanized antibody light chain variable domain
US-10-624-153-94

Query Match 100.0%; Score 576; DB 15; Length 110;
Best Local Similarity 100.0%; Pred. No. 8.4e-41;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTVITCSASODISNYLNMWQOKPKAPKVLITYFTSSLSHSGVPS 60
DB 1 DIQMTSPSSLSASVGDRTVITCSASODISNYLNMWQOKPKAPKVLITYFTSSLSHSGVPS 60

QY 61 RFGSGSGTDFTLTITSSLOPEDPATYCCOQYSTVPMTFGGGTVEIKRTV 110
DB 61 RFGSGSGTDFTLTITSSLOPEDPATYCCOQYSTVPMTFGGGTVEIKRTV 110

RESULT 3
US-09-056-1608-107
Sequence 107, Application US/090561608
Patent No. US20020032315A1

GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,1608
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:

NAME: Haseak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-09-056-1608-107

Query Match 99.5%; Score 573; DB 9; Length 110;
Best Local Similarity 99.1%; Pred. No. 1.5e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTVITCSASODISNYLNMWQOKPKAPKVLITYFTSSLSHSGVPS 60
DB 1 DIQMTSPSSLSASVGDRTVITCSASODISNYLNMWQOKPKAPKVLITYFTSSLSHSGVPS 60

QY 61 RFGSGSGTDFTLTITSSLOPEDPATYCCOQYSTVPMTFGGGTVEIKRTV 110
DB 61 RFGSGSGTDFTLTITSSLOPEDPATYCCOQYSTVPMTFGGGTVEIKRTV 110

RESULT 4
US-09-056-1608-117
Sequence 117, Application US/090561608
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hasek, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-117

Query Match 99.5%; Score 573; DB 9; Length 110;
Best Local Similarity 99.1%; Pred. No. 1.5e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLTNMYQQKPKGAPKVLITYFTSSLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLTNMYQQKPKGAPKVLITYFTSSLHSGVPS 60
Qy 61 RFGSGSGTDFLTITSSLPEDPATYCCQYSTVPTWTFGGTKVEIKRTV 110
Db 61 RFGSGSGTDFLTITSSLPEDPATYCCQYSTVPTWTFGGTKVEIKRTV 110

RESULT 5
US-10-234-671-105
Sequence 105, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856

FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-10-234-671-105

Query Match 99.5%; Score 573; DB 14; Length 110;
Best Local Similarity 99.1%; Pred. No. 1.5e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLTNMYQQKPKGAPKVLITYFTSSLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLTNMYQQKPKGAPKVLITYFTSSLHSGVPS 60
Qy 61 RFGSGSGTDFLTITSSLPEDPATYCCQYSTVPTWTFGGTKVEIKRTV 110
Db 61 RFGSGSGTDFLTITSSLPEDPATYCCQYSTVPTWTFGGTKVEIKRTV 110

RESULT 6
US-10-234-671-115
Sequence 115, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:

LENGTH: 110 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-10-234-671-115

Query Match 99.5%; Score 573; DB 14; Length 110;
Best Local Similarity 99.1%; Pred. No. 1.5e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGDRTVITCSASODISNYLNMWYQKPGKAPKVLITYFTSSLHSGVPS 60
DB 1 DIQWTQSPSSLSASVGDRTVITCSASODISNYLNMWYQKPGKAPKVLITYFTSSLHSGVPS 60
QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCQOYSTVPMWTFGGGTKEIKRTV 110
DB 61 RFGSGSGTDFLTITSSLOPEDFATYYCQOYSTVPMWTFGGGTKEIKRTV 110

RESULT 7
US-10-379-392-135
Sequence 135, Application US/10379392
Publication No. US20040110226A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjarlais, John Rudolf
APPLICANT: Marshall, Shannon Alicia
APPLICANT: Dahiyat, Basel I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR FILING DATE: 2002-05-29
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
SEQ ID NO 135
LENGTH: 213
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Humanized
US-10-379-392-135

Query Match 99.5%; Score 573; DB 16; Length 213;
Best Local Similarity 99.1%; Pred. No. 2.8e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGDRTVITCSASODISNYLNMWYQKPGKAPKVLITYFTSSLHSGVPS 60
DB 1 DIQWTQSPSSLSASVGDRTVITCSASODISNYLNMWYQKPGKAPKVLITYFTSSLHSGVPS 60
QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCQOYSTVPMWTFGGGTKEIKRTV 110
DB 61 RFGSGSGTDFLTITSSLOPEDFATYYCQOYSTVPMWTFGGGTKEIKRTV 110

RESULT 8
US-10-379-392-137
Sequence 137, Application US/10379392
Publication No. US20040110226A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjarlais, John Rudolf
APPLICANT: Marshall, Shannon Alicia
APPLICANT: Dahiyat, Basel I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843

PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR FILING DATE: 2002-05-29
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
SEQ ID NO 137
LENGTH: 213
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-379-392-137

Query Match 99.5%; Score 573; DB 16; Length 213;
Best Local Similarity 99.1%; Pred. No. 2.8e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGDRTVITCSASODISNYLNMWYQKPGKAPKVLITYFTSSLHSGVPS 60
DB 1 DIQWTQSPSSLSASVGDRTVITCSASODISNYLNMWYQKPGKAPKVLITYFTSSLHSGVPS 60
QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCQOYSTVPMWTFGGGTKEIKRTV 110
DB 61 RFGSGSGTDFLTITSSLOPEDFATYYCQOYSTVPMWTFGGGTKEIKRTV 110

RESULT 9
US-10-379-392-139
Sequence 139, Application US/10379392
Publication No. US20040110226A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjarlais, John Rudolf
APPLICANT: Marshall, Shannon Alicia
APPLICANT: Dahiyat, Basel I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR FILING DATE: 2002-05-29
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
SEQ ID NO 139
LENGTH: 213
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (116)..(116)
OTHER INFORMATION: Xaa at position 116 can be Phe or Tyr
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (133)..(133)
OTHER INFORMATION: Xaa at position 133 can be Ile, Met or Val
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (135)..(135)
OTHER INFORMATION: Xaa at position 135 can be Leu, Ile or Met
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (176)..(176)
OTHER INFORMATION: Xaa at position 176 can be Met, Val, Ala or Ser
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (178)..(178)
OTHER INFORMATION: Xaa at position 178 can be Met, Thr or Val
US-10-379-392-139

Query Match 99.5%; Score 573; DB 16; Length 213;
Best Local Similarity 99.1%; Pred. No. 2.8e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTGSSSLASVGDRTVITCSASODISNYLNMWYQKPKAKPKVLIYFTSLHSGVPS 60
DB 1 DIQMTGSSSLASVGDRTVITCSASODISNYLNMWYQKPKAKPKVLIYFTSLHSGVPS 60

QY 61 RFGSGSGTDFTLTTLISLQPEDFATYCCQYSTVPMTFGGTKEIKRTV 110
DB 61 RFGSGSGTDFTLTTLISLQPEDFATYCCQYSTVPMTFGGTKEIKRTV 110

RESULT 10
US-10-364-953-1
Sequence 1, Application US/10364953
Publication No. US20030224397A1
GENERAL INFORMATION:
APPLICANT: LOWMAN, HENRY B.
TITLE OF INVENTION: ANTIBODY VARIANTS WITH FASTER ANTIGEN ASSOCIATION RATES
FILE REFERENCE: PI951R1
CURRENT APPLICATION NUMBER: US/10/364,953
CURRENT FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US 60/355,895
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/409,685
PRIOR FILING DATE: 2002-09-10
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 1
LENGTH: 214
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: Artificial Sequence
LOCATION: Full
OTHER INFORMATION: Y0101-VL
US-10-364-953-1

Query Match 99.5%; Score 573; DB 15; Length 214;
Best Local Similarity 99.1%; Pred. No. 2.8e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTGSSSLASVGDRTVITCSASODISNYLNMWYQKPKAKPKVLIYFTSLHSGVPS 60
DB 1 DIQMTGSSSLASVGDRTVITCSASODISNYLNMWYQKPKAKPKVLIYFTSLHSGVPS 60

QY 61 RFGSGSGTDFTLTTLISLQPEDFATYCCQYSTVPMTFGGTKEIKRTV 110
DB 61 RFGSGSGTDFTLTTLISLQPEDFATYCCQYSTVPMTFGGTKEIKRTV 110

RESULT 11
US-10-020-786-10
Sequence 10, Application US/10020786
Publication No. US20030073164A1
GENERAL INFORMATION:
APPLICANT: Simmons, Laura C.
APPLICANT: Klimowski, Laura
APPLICANT: Reilly, Dorothea
APPLICANT: Yansura, Daniel G.
TITLE OF INVENTION: PROKARYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF
FILE REFERENCE: PI793R1
CURRENT APPLICATION NUMBER: US/10/020,786
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/256,164
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 10
LENGTH: 237
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:

OTHER INFORMATION: anti-VEGF light chain
US-10-020-786-10

Query Match 99.5%; Score 573; DB 14; Length 237;
Best Local Similarity 99.1%; Pred. No. 3.1e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTGSSSLASVGDRTVITCSASODISNYLNMWYQKPKAKPKVLIYFTSLHSGVPS 60
DB 24 DIQMTGSSSLASVGDRTVITCSASODISNYLNMWYQKPKAKPKVLIYFTSLHSGVPS 83

QY 61 RFGSGSGTDFTLTTLISLQPEDFATYCCQYSTVPMTFGGTKEIKRTV 110
DB 84 RFGSGSGTDFTLTTLISLQPEDFATYCCQYSTVPMTFGGTKEIKRTV 133

RESULT 12
US-10-697-995-8
Sequence 8, Application US/10697995
Publication No. US20050048572A1
GENERAL INFORMATION:
APPLICANT: Reilly, Dorothea
APPLICANT: Yansura, Daniel G.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INCREASING ANTIBODY PRODUCTION
FILE REFERENCE: 11669.195USU1
CURRENT APPLICATION NUMBER: US/10/697,995
CURRENT FILING DATE: 2003-10-30
PRIOR APPLICATION NUMBER: US 60/422,952
PRIOR FILING DATE: 2002-10-31
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 8
LENGTH: 237
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: anti-VEGF light chain
US-10-697-995-8

Query Match 99.5%; Score 573; DB 17; Length 237;
Best Local Similarity 99.1%; Pred. No. 3.1e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTGSSSLASVGDRTVITCSASODISNYLNMWYQKPKAKPKVLIYFTSLHSGVPS 60
DB 24 DIQMTGSSSLASVGDRTVITCSASODISNYLNMWYQKPKAKPKVLIYFTSLHSGVPS 83

QY 61 RFGSGSGTDFTLTTLISLQPEDFATYCCQYSTVPMTFGGTKEIKRTV 110
DB 84 RFGSGSGTDFTLTTLISLQPEDFATYCCQYSTVPMTFGGTKEIKRTV 133

RESULT 13
US-10-697-995-11
Sequence 11, Application US/10697995
Publication No. US20050048572A1
GENERAL INFORMATION:
APPLICANT: Reilly, Dorothea
APPLICANT: Yansura, Daniel G.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INCREASING ANTIBODY PRODUCTION
FILE REFERENCE: 11669.195USU1
CURRENT APPLICATION NUMBER: US/10/697,995
CURRENT FILING DATE: 2003-10-30
PRIOR APPLICATION NUMBER: US 60/422,952
PRIOR FILING DATE: 2002-10-31
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 11
LENGTH: 237
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Anti-VEGF light chain
US-10-697-995-11

Query Match 99.5%; Score 573; DB 17; Length 237;
Best Local Similarity 99.1%; Pred. No. 3.1e-40;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASODISNYLNMWYQKPKAPKVLITYFTSSLSHGVPS 60
DB 24 DIQMTQSPSSLSASVGRVTITCSASODISNYLNMWYQKPKAPKVLITYFTSSLSHGVPS 83
QY 61 RFSGSGSGTDFTLTITSSLPEDFATYYCOQYSTVPMWTFGGGTKEIKRTV 110
DB 84 RFSGSGSGTDFTLTITSSLPEDFATYYCOQYSTVPMWTFGGGTKEIKRTV 133

RESULT 14
US-09-056-160B-105
Sequence 105, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Loman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056.160B
FILING DATE: 06-APR-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haasek, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-105

Query Match 99.0%; Score 570; DB 9; Length 110;
Best Local Similarity 98.2%; Pred. No. 2.7e-40;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASODISNYLNMWYQKPKAPKVLITYFTSSLSHGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCSASODISNYLNMWYQKPKAPKVLITYFTSSLSHGVPS 60
QY 61 RFSGSGSGTDFTLTITSSLPEDFATYYCOQYSTVPMWTFGGGTKEIKRTV 110
DB 61 RFSGSGSGTDFTLTITSSLPEDFATYYCOQYSTVPMWTFGGGTKEIKRTV 110

RESULT 15
US-10-234-671-103

Sequence 103, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Loman, Henry B.
APPLICANT: Chen, Yvonne M.

TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-10-234-671-103

Query Match 99.0%; Score 570; DB 14; Length 110;
Best Local Similarity 98.2%; Pred. No. 2.7e-40;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASODISNYLNMWYQKPKAPKVLITYFTSSLSHGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCSASODISNYLNMWYQKPKAPKVLITYFTSSLSHGVPS 60
QY 61 RFSGSGSGTDFTLTITSSLPEDFATYYCOQYSTVPMWTFGGGTKEIKRTV 110
DB 61 RFSGSGSGTDFTLTITSSLPEDFATYYCOQYSTVPMWTFGGGTKEIKRTV 110

Search completed: March 14, 2005, 20:42:12
Job time: 42.0088 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2005, 20:39:29 ; Search time 16.6447 Seconds
(without alignments)
635.867 Million cell updates/sec

Title: US-09-723-752B-8

Perfect score: 576
Sequence: 1 DIQMTQSPSSLSASVGRVT.....YSTVPMTFGGGTKEIKRTV 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	513	89.1	127	2 S40367	Ig kappa chain V-J
2	490	85.1	108	1 KIHUV	Ig kappa chain V-I
3	486	84.4	125	2 S40333	Ig kappa chain V-J
4	485	84.2	123	2 S40331	Ig kappa chain - h
5	484	84.0	108	2 S49047	Ig kappa chain V-J
6	484	84.0	131	2 S40352	Ig kappa chain V-J
7	482	83.7	108	2 S44132	Ig kappa chain V-J
8	482	83.7	109	2 S41938	Ig kappa chain V-J
9	480	83.3	129	2 S52769	Ig kappa chain V-J
10	476	82.6	129	2 S40369	Ig kappa chain - h
11	475	82.5	107	2 S36264	Ig kappa chain V
12	474	82.3	108	1 KIHUV	Ig kappa chain V-I
13	472	81.9	108	1 KIHUV	Ig kappa chain V-I
14	472	81.9	109	2 S31981	Ig kappa chain - h
15	472	81.9	111	2 S48740	Ig kappa chain V-J
16	471.5	81.9	124	2 S40336	Ig kappa chain V-J
17	470	81.6	110	2 S44118	Ig kappa chain V-J
18	469	81.4	108	1 KIHUV	Ig kappa chain V-I
19	469	81.4	139	2 S40365	Ig kappa chain - h
20	468.5	81.3	107	2 S36275	Ig kappa chain V
21	468	81.2	108	2 S19674	Ig kappa chain V
22	468	81.2	132	2 S40334	Ig kappa chain - h
23	467	81.1	108	1 KIHUV	Ig kappa chain V-I
24	467	81.1	125	2 S40339	Ig kappa chain V-J
25	466	80.9	130	2 S40368	Ig kappa chain - h
26	464	80.6	108	2 T39154	Ig kappa chain (BR
27	464	80.6	111	2 E38740	Ig kappa chain V-J
28	462	80.2	108	1 KIHUV	Ig kappa chain V-I
29	462	80.2	108	1 KIHUV	Ig kappa chain V-I

30	462	80.2	111	2 C38740	Ig kappa chain V r
31	462	80.2	122	2 S40314	Ig kappa chain - h
32	462	80.2	129	2 S40317	Ig kappa chain - h
33	462	80.2	129	2 S52793	Ig kappa chain V r
34	462	80.2	135	2 S24320	Ig kappa chain pre
35	461	80.0	108	2 S24382	Ig kappa chain - h
36	460.5	79.9	125	2 S40315	Ig kappa chain - h
37	460	79.9	107	2 S36269	Ig kappa chain V
38	460	79.9	117	2 S46371	Ig kappa chain V-J
39	460	79.9	125	2 S40316	Ig kappa chain - h
40	460	79.9	129	1 KIHUV	Ig kappa chain pre
41	459	79.7	111	2 G38740	Ig kappa chain V r
42	459	79.7	117	2 S46376	Ig kappa chain V-J
43	459	79.7	122	2 S40370	Ig kappa chain - h
44	458	79.5	107	2 L69017	anti-HIV envelope
45	458	79.5	108	1 KIHUV	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

S40367
Ig kappa chain V-J-C region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40367
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40367
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-127 <KLE>
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/33-107/Domain: immunoglobulin homology <IMM>

Query Match 89.1%; Score 513; DB 2; Length 127;
Best Local Similarity 90.0%; Pred. No. 1.9e-38;
Matches 99; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Oy	1	DIQMTQSPSSLSASVGRVTITCSASODISNINLNTQKRGKAPKULIYFTSSLSGVS	60
Db	18	DIQMTQSPSSLSASVGRVTITCRASQISININLNTQKRGKAPKULIYASSLSGVS	77
Oy	61	RFGSGSGTDFLTITISLOPEDPATYCCOYSTVPMTFGGGTKEIKRTV	110
Db	78	RFGSGSGTDFLTITISLOPEDPATYCCOYSTVPMTFGGGTKEIKRTV	127

RESULT 2

KIHUV
Ig kappa chain V-I region (Au) - human
C/Species: Homo sapiens (man)
C/Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C/Accession: A91653; A01862; S02573
R/Schlickehl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A/Title: Die Primärstruktur einer monoklonalen Immunoglobulin-L-Kette vom kappa-Typ, Su
A/Reference number: A91653; MUID:72189444; PMID:5028201
A/Accession: A91653
A/Molecule type: protein
A/Residues: 1-108 <SCH>
A/Cross-references: UNIPROT:P01594
A/Note: The C region of this chain has the Inv (3) marker
R/Phlanner, H.; Schiffer, M.; Bep, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; Ste
Biophys. Struct. Mech. 1, 139-146, 1975
A/Title: The structure determination of the variable portion of the Bence-Jones protein
A/Reference number: A90729; MUID:77022433; PMID:1234024
A/Contents: annotation; X-ray crystallography

A/Note: the structure of the V region was determined by molecular replacement methods using R/Stefner, V.; Chang, J.Y.
 PDB: 222, 6-10, 1987
 A/Title: Chemical modification of the carboxyl groups of protein substrates enhances the A/Reference number: S02572; MUID:8805152; PMID:3115831
 A/Content: annotation
 C/Comment: This is a Bence Jones protein.
 C/Genetic: GDB:IGKVL
 A/Cross-references: GDB:136264
 A/Map position: 2p12-2p12
 C/Complex: an immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds in some cases, such as Iga and Igm, the subunits associate into 16 C/KeyWords: heterotrimer; immunoglobulin
 F/16-90/Domain: immunoglobulin homology <IMM>
 F/23-88/Disulfide bonds: #status predicted

Query Match 85.1%; Score 490; DB 1; Length 108;
 Best Local Similarity 86.1%; Pred. No. 1.7e-36;
 Matches 93; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGRVITTCASODISNYLMWYQKPKAPKVLITYFTSLHSGVPS 60
 DB 1 DIQMTSPSSLSASVGRVITTCASODISNYLMWYQKPKAPKVLITYFTSLHSGVPS 60
 QY 61 RFGSGSGTDFTLTISLQPEDFATYYCOQYSTVPMTFGGTVEIKR 108
 DB 61 RFGSGSGTDFTLTISLQPEDFATYYCOQYSTVPMTFGGTVEIKR 108

RESULT 3

S40333
 Ig kappa chain V-J region - human
 A/Species: Homo sapiens (man)
 C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40333
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chl genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341
 A/Accession: S40333
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-125 <KLB>
 A/Cross-references: EMBL:X72443; NID:G441354; PIDN:CAAS111.1; PID:G441355
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/KeyWords: heterotrimer; immunoglobulin
 F/34-108/Domain: immunoglobulin homology <IMM>

Query Match 84.4%; Score 486; DB 2; Length 125;
 Best Local Similarity 86.0%; Pred. No. 4.5e-36;
 Matches 92; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGRVITTCASODISNYLMWYQKPKAPKVLITYFTSLHSGVPS 60
 DB 19 DIQMTSPSSLSASVGRVITTCASODISNYLMWYQKPKAPKVLITYFTSLHSGVPS 78
 QY 61 RFGSGSGTDFTLTISLQPEDFATYYCOQYSTVPMTFGGTVEIKR 107
 DB 79 RFGSGSGTDFTLTISLQPEDFATYYCOQYSTVPMTFGGTVEIKR 125

RESULT 4

S40331
 Ig kappa chain - human
 A/Species: Homo sapiens (man)
 C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40331
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chl genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341

A/Accession: S40331
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-123 <KLB>
 A/Cross-references: EMBL:X72441; NID:G441350; PIDN:CAAS1109.1; PID:G441351
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/KeyWords: heterotrimer; immunoglobulin
 F/32-106/Domain: immunoglobulin homology <IMM>

Query Match 84.2%; Score 485; DB 2; Length 123;
 Best Local Similarity 88.8%; Pred. No. 5.4e-36;
 Matches 95; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGRVITTCASODISNYLMWYQKPKAPKVLITYFTSLHSGVPS 60
 DB 17 DIQMTSPSSLSASVGRVITTCASODISNYLMWYQKPKAPKVLITYFTSLHSGVPS 76
 QY 61 RFGSGSGTDFTLTISLQPEDFATYYCOQYSTVPMTFGGTVEIKR 107
 DB 77 RFGSGSGTDFTLTISLQPEDFATYYCOQYSTVPMTFGGTVEIKR 123

RESULT 5

B49047
 Ig kappa chain V region (monoclonal strational autoantibody strAB SA-1A) - human (frag
 A/Species: Homo sapiens (man)
 C/Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C/Accession: B49047
 R/Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
 Eur. J. Immunol. 22, 2231-2236, 1992
 A/Title: Human monoclonal strational autoantibodies isolated from thymic B lymphocytes
 A/Reference number: A49047; MUID:92387224; PMID:1316616
 A/Accession: B49047
 A/Status: preliminary
 A/Molecule type: nucleic acid
 A/Residues: 1-108 <VIC>
 A/Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77
 A/Experimental source: thymic B lymphocytes
 A/Note: sequence extracted from NCBI Backbone (NCBIN:113208, NCBI:113209)
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.0%; Score 484; DB 2; Length 108;
 Best Local Similarity 88.0%; Pred. No. 5.8e-36;
 Matches 95; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGRVITTCASODISNYLMWYQKPKAPKVLITYFTSLHSGVPS 60
 DB 1 DIQMTSPSSLSASVGRVITTCASODISNYLMWYQKPKAPKVLITYFTSLHSGVPS 60
 QY 61 RFGSGSGTDFTLTISLQPEDFATYYCOQYSTVPMTFGGTVEIKR 108
 DB 61 RFGSGSGTDFTLTISLQPEDFATYYCOQYSTVPMTFGGTVEIKR 108

RESULT 6

S40352
 Ig kappa chain V-J-C region - human
 A/Species: Homo sapiens (man)
 C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40352
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chl genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341
 A/Accession: S40352
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-131 <KLB>
 A/Cross-references: EMBL:X72462; NID:G441392; PIDN:CAAS1130.1; PID:G441393
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/KeyWords: heterotrimer; immunoglobulin
 F/36-110/Domain: immunoglobulin homology <IMM>

Query Match 84.0%; Score 484; DB 2; Length 131;
 Best Local Similarity 85.5%; Pred. No. 7.1e-36;
 Matches 94; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTVITTCASQDISNLYLMWYQKRGKAPKVLIFTSSLSHGVS 60
 |||
 DB 21 DIOMTQSPSSLSASVGDRTVITTCASQDISNLYLMWYQKRGKAPKVLIFTSSLSHGVS 80
 |||
 QY 61 RFSGSGSGTDFTLTISLQPEDFATYYCQOYSTVPMTFGGTVEIKRTV 110
 |||
 DB 81 RFSGSGSGTDFTLTISLQPEDFATYYCQKXNSVPRFGGTVEIKRTV 130
 |||

RESULT 7

844122
 Ig kappa chain V region - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_rev13-Jan-1995 #text_change 24-May-2001
 C/Accession: S44122
 R/Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
 Submitted to the EMBL Data Library, March 1994
 A/Description: Idiotype vaccination against human B-cell lymphoma: rescue of variable
 A/Reference number: S44105
 A/Accession: S44122
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-108 <HAM>
 A/Cross-references: EMBL:231390; NID:9472976; PIDN:CAA83265.1; PID:9940533
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.7%; Score 482; DB 2; Length 108;
 Best Local Similarity 87.0%; Pred. No. 8.7e-36;
 Matches 94; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTVITTCASQDISNLYLMWYQKRGKAPKVLIFTSSLSHGVS 60
 |||
 DB 1 DIOMTQSPSSLSASVGDRTVITTCASQDISNLYLMWYQKRGKAPKVLIFTSSLSHGVS 60
 |||
 QY 61 RFSGSGSGTDFTLTISLQPEDFATYYCQOYSTVPMTFGGTVEIKR 108
 |||
 DB 61 RFSGSGSGTDFTLTISLQPEDFATYYCQOYSTVPMTFGGTVEIKR 108
 |||

RESULT 8

S31998
 Ig kappa chain - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 06-Feb-1995 #sequence_rev13-Jan-1995 #text_change 21-Jan-2000
 C/Accession: S31998
 R/Portolano, S.; Chazenbalk, G.D.; Hutcheson, S.J.; McLachlan, S.M.; Rapoport, B.
 Submitted to the EMBL Data Library, June 1992
 A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
 A/Reference number: S31977
 A/Accession: S31998
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-109 <FOR>
 A/Cross-references: EMBL:215081; NID:938501; PIDN:CAA78790.1; PID:938502
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.7%; Score 482; DB 2; Length 109;
 Best Local Similarity 85.3%; Pred. No. 8.8e-36;
 Matches 93; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTVITTCASQDISNLYLMWYQKRGKAPKVLIFTSSLSHGVS 60
 |||
 DB 1 ELMVTQSPSSLSASVGDRTVITTCASQDISNLYLMWYQKRGKAPKVLIFTSSLSHGVS 60
 |||

QY 61 RFSGSGSGTDFTLTISLQPEDFATYYCQOYSTVPMTFGGTVEIKRT 109
 |||
 DB 61 RFSGSGSGTDFTLTISLQPEDFATYYCQOYSTVPMTFGGTVEIKRT 109
 |||

RESULT 9

S52789
 Ig kappa chain V region - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 19-May-1995 #sequence_rev13-Jan-1995 #text_change 21-Jan-2000
 C/Accession: S52789
 R/Rocca, A.; Khamilchi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Deret,
 submitted to the EMBL Data Library, March 1995
 A/Description: light chain V region gene usage restriction and peculiarities in myeloma-
 A/Reference number: S52789
 A/Accession: S52789
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-129 <ROC>
 A/Cross-references: EMBL:X85995; NID:9758588; PIDN:CAA59987.1; PID:9758589
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/38-112/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 480; DB 2; Length 129;
 Best Local Similarity 86.0%; Pred. No. 1.6e-35;
 Matches 92; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTVITTCASQDISNLYLMWYQKRGKAPKVLIFTSSLSHGVS 60
 |||
 DB 23 DIOMTQSPSSLSASVGDRTVITTCASQDISNLYLMWYQKRGKAPKVLIFTSSLSHGVS 82
 |||
 QY 61 RFSGSGSGTDFTLTISLQPEDFATYYCQOYSTVPMTFGGTVEIK 107
 |||
 DB 83 RFSGSGSGTDFTLTISLQPEDFATYYCQOYSTVPMTFGGTVEIK 129
 |||

RESULT 10

S40369
 Ig kappa chain - human
 C/Species: Homo sapiens (man)
 C/Date: 06-Mar-1994 #sequence_rev13-Jan-1995 #text_change 21-Jan-2000
 C/Accession: S40369
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin ch1 genes and their hypermutation.
 A/Reference number: S40312; MID:9408091; PMID:8258341
 A/Accession: S40369
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-129 <KLE>
 A/Cross-references: EMBL:X72479; NID:9441426; PIDN:CAA51147.1; PID:9441427
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/37-11/Domain: immunoglobulin homology <IMM>

Query Match 82.6%; Score 476; DB 2; Length 129;
 Best Local Similarity 85.2%; Pred. No. 3.5e-35;
 Matches 92; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTVITTCASQDISNLYLMWYQKRGKAPKVLIFTSSLSHGVS 60
 |||
 DB 22 DIOMTQSPSSLSASVGDRTVITTCASQDISNLYLMWYQKRGKAPKVLIFTSSLSHGVS 81
 |||

QY 61 RFSGSGSGTDFTLTISLQPEDFATYYCQOYSTVPMTFGGTVEIKR 108
 |||
 DB 82 RFSGSGSGTDFTLTISLQPEDFATYYCQOYSTVPMTFGGTVEIKR 129
 |||

RESULT 11

S36264
 Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)
 C/Species: Homo sapiens (man)

Ig kappa chain V region (Py20) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
 C:Accession: A38740
 R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
 J. Biol. Chem. 266, 6607-6613, 1991
 A>Title: Heavy and light chain variable region sequences and antibody properties of anti-
 A:Reference number: A38740; MUID:91177923; PMID:1706720
 A:Accession: A38740
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A:Molecule type: mRNA
 A:Residues: 1-111 <RUF>
 A:Cross-references: UNIPROT:Q91WS9
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 81.9%; Score 472; DB 2; Length 111;
 Best Local Similarity 81.5%; Pred. No. 6.8e-35;
 Matches 88; Conservative 11; Mismatches 9; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVTITCSASODISNYLNMWYQOKPKARKTLITFTSLHSGVPS 60
 DB 4 DVQMTQTITSSLSASLGRVTISCSASQGISNYLNMWYQOKPKDGTVKLLIYTSSLSHSGVPS 63
 QY 61 RPSGSGSGTDFLTITISLQPEDFATYYCOQYSTVPWTFGQTFVEIKR 108
 DB 64 RPSGSGSGTDYSLTISNLEPEDVATYYCOQYSTVPWTFGQTKLEIKR 111

Search completed: March 14, 2005, 21:08:51
 Job time : 17.6447 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2005, 20:32:33 ; Search time 77.193 Seconds

(without alignment)
729.713 Million cell updates/sec

Title: US-09-723-752b-8
Perfect score: 576
Sequence: 1 DIQWTQSPSSLSASVGRVT.....YSTVPMTFGCCTKYIKRTV 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing filter 45 summaries

Database :

1: uniprot_03:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	490	85.1	108	1 KY1B_HUMAN	P01594 homo sapien
2	488	84.7	108	09UL77	Q9UL77 homo sapien
3	485	84.4	236	06GKX9	Q6GKX9 homo sapien
4	485	84.2	236	06GKX1	Q6GKX1 homo sapien
5	484	84.0	236	07Z3Y4	Q7Z3Y4 homo sapien
6	477.5	82.9	107	2 Q6S8A9	Q6S8A9 homo sapien
7	477	82.8	236	2 Q6GKX8	Q6GKX8 homo sapien
8	474	82.3	108	1 KY1H_HUMAN	P01600 homo sapien
9	474	82.3	108	1 KY1Y_HUMAN	P01600 homo sapien
10	474	82.3	236	2 Q6GKX0	Q6GKX0 homo sapien
11	472	81.9	108	1 KY1R_HUMAN	P01607 homo sapien
12	469	81.4	108	1 KY1U_HUMAN	Q9UL70 homo sapien
13	468	81.2	108	2 Q9UL70	Q9UL70 homo sapien
14	467	81.1	108	1 KY1A_HUMAN	P01593 homo sapien
15	465	80.7	234	2 Q7Z473	Q7Z473 homo sapien
16	463	80.4	236	2 Q6PIH7	Q6PIH7 homo sapien
17	462	80.2	108	1 KY1P_HUMAN	P01608 homo sapien
18	462	80.2	108	1 KY1V_HUMAN	P01607 homo sapien
19	460	79.9	129	1 KY1W_HUMAN	P01607 homo sapien
20	458	79.5	108	1 KY1D_HUMAN	P01597 homo sapien
21	457.5	79.4	107	1 KY1D_HUMAN	P01596 homo sapien
22	457	79.3	108	1 KY1M_HUMAN	P01605 homo sapien
23	456	79.2	108	1 KY1K_HUMAN	P01603 homo sapien
24	455.5	79.0	244	2 Q6S2C8	Q6S2C8 homo sapien
25	455	79.0	244	2 Q6S2C8	Q6S2C8 homo sapien
26	452	78.5	108	1 KY1O_HUMAN	P01609 homo sapien
27	451	78.3	108	1 KY1S_HUMAN	P01611 homo sapien
28	451	78.3	116	2 Q96PF6	Q96PF6 homo sapien
29	450	78.1	108	1 KY1N_HUMAN	P01606 homo sapien
30	449	78.0	108	1 KY1C_HUMAN	P01595 homo sapien
31	448	77.8	108	1 KY1J_MOUSE	P01643 mus musculu

32	448	77.8	240	2 Q6S2C9	Q6S2C9 homo sapien
33	446	77.4	108	1 KY1G_HUMAN	P01599 homo sapien
34	443	76.9	236	2 Q6PIF5	Q6PIF5 homo sapien
35	442	76.7	108	1 KY1F_HUMAN	P01598 homo sapien
36	442	76.7	108	1 KY1L_HUMAN	Q9UL79 homo sapien
37	442	76.7	108	2 Q9UL79	Q9UL79 homo sapien
38	441	76.6	236	2 Q6PIH4	Q6PIH4 homo sapien
39	431	74.8	108	1 KY5K_MOUSE	P01644 mus musculu
40	431	74.8	108	1 KY5N_MOUSE	P01647 mus musculu
41	429	74.5	108	1 KY5L_MOUSE	P01645 mus musculu
42	429	74.5	108	1 KY5M_MOUSE	P01646 mus musculu
43	428	74.3	108	1 KY5O_MOUSE	P01648 mus musculu
44	427.5	74.2	109	1 KY1T_HUMAN	P01612 homo sapien
45	425	73.8	108	1 KY5U_MOUSE	P04946 mus musculu

ALIGNMENTS

RESULT 1
ID KY1B_HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 19 kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schliehl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=77022433; PubMed=1234024;
RA Fehllhammer H., Schiffer M., Bpp O., Colman P.M., Lattman E.E., Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the Bence-Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -1- MISCELLANEOUS: The structure of the V region was determined by molecular replacement methods using the known structure of the V region of the kappa chain RT.
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC PIR; A91653; K1HUAU.
DR PDB; 1UV5; X-ray; A=1-107.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG_1.
DR PROSITE; PSS0835; IG LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing; Immunoglobulin V region.
KW DOMAIN 1 23
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 2 34 Complementarity-determining-1.
FT DOMAIN 3 35 Framework-2.
FT DOMAIN 4 49 Complementarity-determining-2.
FT DOMAIN 50 56 Complementarity-determining-3.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-4.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT STRAND 4 5

FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 44 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 97 98
FT STRAND 102 106
FT NON_TER 108
SQ SEQUENCE 108 AA; 11939 MW; E801187BE6F6B9 CRC64;

Query Match 85.1%; Score 490; DB 1; Length 108;
Best Local Similarity 86.1%; Pred. No. 1.2e-42;
Matches 93; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIOMTQSPSSLSASVGDRTVITTCASQDISNTLNMVYQKPKAPKVLITYFTSSLSHGVS 60
Db 1 DIOMTQSPSSLSASVGDRTVITTCASQDISNTLNMVYQKPKAPKVLITYDASNLSSGVPS 60
Qy 61 RFGSGSGCTDPTLTITSSLOPEDFATYCCQOYSTVPMFGGKTKEIKR 108
Db 61 RFGSGSGAHFTFTTSSLOPEDFATYCCQOYSTVPMFGGKTKEIKR 108

RESULT 2

Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cjln.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR PIR; B49047; B49047.
DR PIR; B34083; B34083.
DR HSSP; P01607; IBMW.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 84.7%; Score 488; DB 2; Length 108;
Best Local Similarity 87.0%; Pred. No. 2e-42;
Matches 94; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIOMTQSPSSLSASVGDRTVITTCASQDISNTLNMVYQKPKAPKVLITYFTSSLSHGVS 60
Db 1 DIOMTQSPSSLSASVGDRTVITTCASQDISNTLNMVYQKPKAPKVLITYFTSSLSHGVS 60

Db 1 DIOMTQSPSSLSASVGDRTVITTCASQDISNTLNMVYQKPKAPKVLITYFTSSLSHGVS 60
Qy 61 RFGSGSGCTDPTLTITSSLOPEDFATYCCQOYSTVPMFGGKTKEIKR 108
Db 61 RFGSGSGCTDPTLTITSSLOPEDFATYCCQOYSTVPMFGGKTKEIKR 108

RESULT 3

ID Q6GKX9 PRELIMINARY; PRT; 236 AA.
AC Q6GKX9;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge U.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Dichtchenko L., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stepietov M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrin P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bork S.A., McGowan P.T., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman W., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
RA Krzywinski M.I., Skaleck J., Small D.E., Scheraga A., Schein J.E.,
RA Jones S.J., Maitra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strauberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073763; AAH73763.1; -.
DR InterPro; IPR003599; IG_1like.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-sect; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KV Hypothetical protein.
SQ SEQUENCE 236 AA; 25924 MW; PDE2093DC560CF7 CRC64;

Query Match 84.4%; Score 486; DB 2; Length 236;
Best Local Similarity 86.4%; Pred. No. 7.8e-42;
Matches 95; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIOMTQSPSSLSASVGDRTVITTCASQDISNTLNMVYQKPKAPKVLITYFTSSLSHGVS 60
Db 23 DIOMTQSPSSLSASVGDRTVITTCASQDISNTLNMVYQKPKAPKVLITYFTSSLSHGVS 82
Qy 61 RFGSGSGCTDPTLTITSSLOPEDFATYCCQOYSTVPMFGGKTKEIKRTV 110

Db 83 RFSSGSGTDFLTITSLQPEDPATYCCQNTYTLTTCGGTKVEIKRTV 132

```
RESULT 4
ID 06GMW1 PRELIMINARY; PRT; 236 AA.
AC 06GMW1;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bock S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallatton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strauberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -
DR InterPro; IPR003599; IG_1
DR InterPro; IPR007110; IG_1like
DR InterPro; IPR003597; IG_1
DR InterPro; IPR003006; IG_MHC
DR InterPro; IPR003596; IG_V
DR Pfam; PF07654; CI-bet; 1
DR Pfam; PF00047; Ig; 2
DR SMART; SM00409; IG; 2
DR SMART; SM00406; IGV; 1
DR PROSITE; PS00835; IG_LIKE; 2
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;

Query Match 84.2%; Score 485; DB 2; Length 236;
Best Local Similarity 86.1%; Pred. No. 96-42;
Matches 96; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy 2 IQMTQSPSSLSASVGRVTITCSASQDISNYLMTYQKGRKAPKVLITYFTSLHSGVSR 61
Db 24 IQMTQSPSSLSASVGRVTITCSASQDISNYLMTYQKGRKAPKVLITYFTSLHSGVSR 83

Qy 62 RFSSGSGTDFLTITSLQPEDPATYCCQNTYTLTTCGGTKVEIKRTV 110
Db 84 RFSSGSGTDFLTITSLQPEDPATYCCQNTYTLTTCGGTKVEIKRTV 132
```

Db 83 RFSSGSGTDFLTITSLQPEDPATYCCQNTYTLTTCGGTKVEIKRTV 132

```
RESULT 5
ID 0723Y4 PRELIMINARY; PRT; 236 AA.
AC 0723Y4;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bock S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallatton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RA Strauberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AAH05332.1; -
DR HSSP; P01834; 1HEZ
DR InterPro; IPR007110; IG_1like
DR InterPro; IPR003597; IG_1
DR InterPro; IPR003006; IG_MHC
DR InterPro; IPR003596; IG_V
DR Pfam; PF07654; CI-bet; 1
DR SMART; SM00406; IGV; 1
DR PROSITE; PS00835; IG_LIKE; 2
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;

Query Match 84.0%; Score 484; DB 2; Length 236;
Best Local Similarity 86.4%; Pred. No. 1.36-41;
Matches 95; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLMTYQKGRKAPKVLITYFTSLHSGVSR 60
Db 23 DIQMTQSPSSLSASVGRVTITCSASQDISNYLMTYQKGRKAPKVLITYFTSLHSGVSR 82

Qy 61 RFSSGSGTDFLTITSLQPEDPATYCCQNTYTLTTCGGTKVEIKRTV 110
Db 83 RFSSGSGTDFLTITSLQPEDPATYCCQNTYTLTTCGGTKVEIKRTV 132

RESULT 6
ID 096SA9 PRELIMINARY; PRT; 107 AA.
AC 096SA9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
```

01-DEC-2001 (TReMBLrel. 19, last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, last annotation update)
 DE Anti-Streptococcal/anti-mycosin immunoglobulin kappa light chain
 DE variable region (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
 RT "Molecular analysis of polyclonal monoclonal antibodies from
 RT rheumatic carditis: human anti-N-acetylglucosamine/anti-mycosin
 RT antibody V region genes."
 RL J. Immunol. 161:2020-2031 (1998).
 DR EMBL: U96396; AAB68785.1; -
 DR PIR: B49047; B49047.
 DR PIR: PH0867; PH0867.
 DR PIR: S16840; S16840.
 DR PIR: S31977; S31977.
 DR PIR: S34083; S34083.
 DR PIR: S34086; S34086.
 DR HSSP: P01607; 1BMW.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003596; IG_V.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 FT NON_TER 1
 FT TER 1
 SQ SEQUENCE 107 AA; 11520 MW; 4BB43B9C5B577F16 CRC64;

Query Match 82.9%; Score 477.5; DB 2; Length 107;
 Best Local Similarity 89.0%; Pred. No. 2.3e-41;
 Matches 97; Conservative 3; Mismatches 6; Indels 3; Gaps 2;

OY 1 DIQMTGSSSSASVGVDRVTITCSASODISNYLWYQKPKAPKVLTYFTSSLSHGVS 60
 DB 1 DIQMTGSSSSASVGVDRVTITCRASQGISSTYLMWYQKPKAPKVLTYAASLSHGVS 60
 OY 61 RFSSGSGTDPFTLTITSSLOPEDFATYCCQ-QYSTVPMFTFGOSTKYEIKR 108
 DB 61 RFSSGSGTDPFTLTITSSLOPEDFATYCCQ-QYSTVPMFTFGOSTKYEIKR 107

RESULT 7
 O6GMX8 PRELIMINARY; PRT; 236 AA.
 AC O6GMX8:
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Pelting E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares T.B., Bonaldi M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loggiano N.A., Pecere G.J., Abramson R.D., Mullins S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Kravynski M.I., Skalec U., Smallos D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (Jun-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC073764; AAH73764.1; -
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003597; IG_C1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF07654; C1-set; 1.
 DR Pfam: PF00047; IG; 2.
 DR SMART: SM00409; IG; 2.
 DR SMART: SM00407; IGV; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 2.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 25707 MW; 4FC8B14B6559EFC9 CRC64;

Query Match 82.8%; Score 477; DB 2; Length 236;
 Best Local Similarity 84.5%; Pred. No. 6.6e-41;
 Matches 93; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

OY 1 DIQMTGSSSSASVGVDRVTITCSASODISNYLWYQKPKAPKVLTYFTSSLSHGVS 60
 DB 23 DIQMTGSSSSASVGVDRVTITCRASQGISSTYLMWYQKPKAPKVLTYAASLSHGVS 82
 OY 61 RFSSGSGTDPFTLTITSSLOPEDFATYCCQ-QYSTVPMFTFGOSTKYEIKRTV 110
 DB 83 RFSSGSGTDPFTLTITSSLOPEDFATYCCQ-QAHSPFTFGPKVDIKRTV 132

RESULT 8
 K1H1_HUMAN STANDARD; PRT; 108 AA.
 ID K1H1_HUMAN
 AC P01600;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, last sequence update)
 DT 25-OCT-2004 (Rel. 45, last annotation update)
 DS IG kappa chain V-I region Hau.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=71032830; PubMed=4097974;
 RA Watanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
 RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
 RT subgroups."
 RL Hoppe-Seyler G.Z. Physiol. Chem. 351:1291-1295 (1970).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR: A01868; K1H1HU.
 DR PDB: 1P6L; X-ray; L=1-108.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IGV; 1.
 DR SMART: SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.
 KM 3D-structure; Bence-Jones protein; Direct protein sequencing;
 KM Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 107 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;
 Query Match 82.3%; Score 474; DB 1; Length 108;
 Best Local Similarity 86.1%; Pred. No. 5,4e-41;
 Matches 93; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
 QY 1 DIQMTSPSSLSASVGDRTVITCSASODISNYLNMWYQKQKAPKVLITYFTSLHSGVPS 60
 DB 1 DIQMTSPSSLSASVGDRTVITCSASODISNYLNMWYQKQKAPKVLITYFTSLHSGVPS 60
 QY 61 RFSGSGSGTDFTLTISLQPEDPATYCCQYSTVPMTFGGGTVEIKR 108
 DB 61 RFSGSGSGTDFTLTISLQPEDPATYCCQYSTVPMTFGGGTVEIKR 108
 RESULT 9
 KLVY HUMAN STANDARD; PRT; 108 AA.
 ID P80362;
 AC 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE 19 kappa chain V-I region WAT.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 1-35.
 RX MEDLINE=616731; PubMed=616731;
 RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
 RA Popp R.A., Solomon A.;
 RT "Characterization and preliminary crystallographic data on the VL-
 RT related fragment of the human kappa Bence Jones protein Wat.";
 RL J. Mol. Biol. 147:185-193(1981).
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PDB: 1WTL, X-ray; A/B=1-108.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR003110; IG-like.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IgV_1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM 3D-structure; Bence-Jones protein; Direct protein sequencing;
 KM Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.

FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 107 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT CONFLICT 30 31 TN -> SD (in Ref. 2).
 FT STRAND 4 7
 FT STRAND 10 13
 FT TURN 15 16
 FT STRAND 19 25
 FT TURN 30 31
 FT STRAND 33 38
 FT TURN 40 41
 FT STRAND 45 49
 FT TURN 50 52
 FT STRAND 53 54
 FT TURN 56 57
 FT TURN 60 61
 FT STRAND 62 67
 FT TURN 68 69
 FT STRAND 70 75
 FT HELIX 80 82
 FT STRAND 84 90
 FT STRAND 98 98
 FT STRAND 102 106
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;
 Query Match 82.3%; Score 474; DB 1; Length 108;
 Best Local Similarity 83.3%; Pred. No. 5,4e-41;
 Matches 90; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
 QY 1 DIQMTSPSSLSASVGDRTVITCSASODISNYLNMWYQKQKAPKVLITYFTSLHSGVPS 60
 DB 1 DIQMTSPSSLSASVGDRTVITCSASODISNYLNMWYQKQKAPKVLITYFTSLHSGVPS 60
 QY 61 RFSGSGSGTDFTLTISLQPEDPATYCCQYSTVPMTFGGGTVEIKR 108
 DB 61 RFSGSGSGTDFTLTISLQPEDPATYCCQYSTVPMTFGGGTVEIKR 108
 RESULT 10
 Q6GMXO PRELIMINARY; PRT; 236 AA.
 ID Q6GMXO;
 AC 05-JUL-2004 (TRENBLREL, 27, Created)
 DT 05-JUL-2004 (TRENBLREL, 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLREL, 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Splice;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughell N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schnarch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Spleen;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC073775; AAH73775.1; -.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG-11ke.
 DR InterPro: IPR003597; IG C1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF07654; C1-sec; 1.
 DR Pfam: PF00047; IG; 2.
 DR SMART: SM00409; IG; 2.
 DR SMART: SM00407; IGc1; 1.
 DR SMART: SM00406; IG; 1.
 DR PROSITE: PS00835; IG LIKE; 2.
 DR PROSITE: PS00230; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BFA9 CRC64;
 Query Match Best Local Similarity 83.3%; Score 474; DB 2; Length 236;
 Matches 92; Conservative 6; Mismatches 12; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNMYQOKPKAPKVLITYTSSLHSGVPS 60
 DB 23 DIQMTQSPSSLSASVGRVTITCRASQINNNYLNMYQKPKAPKVLITYTSSLHSGVPS 82
 QY 61 RFGSGSGDTFTLTISLQPEDPATYCCQYSTVPTWTFGQGTKEIKR 110
 DB 83 RFGSGSGDTFTLTISLQPEDPATYCCQYSTVPTWTFGQGTKEIKR 132
 RESULT 11
 KVI0_HUMAN STANDARD; PRT; 108 AA.
 ID KVI0_HUMAN
 AC P01610;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update).
 DE Ig kappa chain V-I region WEA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=63273707; PubMed=6410398;
 RA Goni F., Frangione B.;
 RT "Amino acid sequence of the Fv region of a human monoclonal IgM
 (protein WEA) with antibody activity against 3,4-pyruvylated galactose
 in Klebsiella polysaccharides K30 and K33".
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
 CC -1- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
 against 3,4-pyruvylated galactose and isolated from a patient with
 Waldenstrom's macroglobulinemia.
 DR PIR: A01876; KIHUME.
 DR HSSP: P80362; 1WTL.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; P:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-11ke.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG; 1.
 DR SMART: SM00406; IG; 1.
 DR PROSITE: PS00835; IG LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin V region;
 KM Monoclonal antibody.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.

FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 107 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;
 Query Match Best Local Similarity 81.9%; Score 472; DB 1; Length 108;
 Matches 91; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNMYQOKPKAPKVLITYTSSLHSGVPS 60
 DB 1 DIQMTQSPSSLSASVGRVTITCRASQGRNDLTWYQOKPKAPKVLITYTSSLHSGVPS 60
 QY 61 RFGSGSGDTFTLTISLQPEDPATYCCQYSTVPTWTFGQGTKEIKR 108
 DB 61 RFGSGSGDTFTLTISLQPEDPATYCCQYSTVPTWTFGQGTKEIKR 108
 RESULT 12
 KVI0_HUMAN STANDARD; PRT; 108 AA.
 ID KVI0_HUMAN
 AC P01607;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig kappa chain V-I region Rel.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76023758; PubMed=809329;
 RA Palm W., Hilschmann N.;
 RT "The primary structure of a crystalline monoclonal immunoglobulin
 kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation
 and characterization of the tryptic peptides; the complete amino acid
 sequence of the protein; a contribution to the elucidation of the
 three-dimensional structure of antibodies, in particular their
 combining site.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=76039968; PubMed=1182131;
 RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
 RT "The molecular structure of a dimer composed of the variable portions
 of the Bence-Jones protein Rel refined at 2.0-A resolution.";
 RL Biochemistry 14:4943-4952(1975).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
 marker.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR: A91663; KIHURS.
 DR PDB: 1AR2; X-ray; @=1-107.
 DR PDB: 1BWI; X-ray; A/B=1-107.
 DR PDB: 1REI; X-ray; A/B=1-107.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; P:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-11ke.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG; 1.
 DR SMART: SM00406; IG; 1.
 DR PROSITE: PS00835; IG LIKE; 1.
 KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
 KM Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.

FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DISULFID 98 107 Framework-4.
 FT STRAND 23 88
 FT STRAND 4 7
 FT STRAND 10 13
 FT TURN 15 16
 FT STRAND 19 25
 FT TURN 30 31
 FT STRAND 33 38
 FT TURN 40 41
 FT STRAND 45 49
 FT TURN 50 52
 FT STRAND 53 54
 FT TURN 56 57
 FT TURN 60 61
 FT STRAND 62 67
 FT TURN 68 69
 FT STRAND 70 75
 FT HELIX 80 82
 FT STRAND 84 90
 FT STRAND 97 98
 FT STRAND 102 106
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 81.4%; Score 469; DB 1; Length 108;
 Best Local Similarity 81.5%; Pred. No. 1.8e-40;
 Matches 88; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITTCASQDISNLYNMYOQKPKAKYLYFTSSLHSGVPS 60
 Db 1 DIQMTQSPSSLSASVGDRTVITTCASQDISNLYNMYOQKPKAKYLYFTSSLHSGVPS 60
 61 RFSGSGSGTDFLTITSLQPEDPATYTCQOYSTVPMPTFGGKVEIKR 108
 Db 61 RFSGSGSGTDFLTITSLQPEDPATYTCQOYSTVPMPTFGGKVEIKR 108

RESULT 13

Qy 09UL70 PRELIMINARY; PRT; 108 AA.
 AC 09UL70;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
 RA Wu X., Liu B., Van der Merwe P.L., Kalle N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RT Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL, AF035044, AAD56280.1; -.
 DR PIR, PH0863; PH0863.
 DR HSSP, P01607; 1BMW.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003586; IG-V.
 DR SMART, SM00406; IGV, 1.
 DR PROSITE, PS50835; IG-LIKE; 1.
 FT NON_TER 1 1
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 81.2%; Score 468; DB 2; Length 108;
 Best Local Similarity 84.3%; Pred. No. 2.2e-40;

Matches 91; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
 Qy 1 DIQMTQSPSSLSASVGDRTVITTCASQDISNLYNMYOQKPKAKYLYFTSSLHSGVPS 60
 Db 1 DIQMTQSPSSLSASVGDRTVITTCASQDISNLYNMYOQKPKAKYLYFTSSLHSGVPS 60
 61 RFSGSGSGTDFLTITSLQPEDPATYTCQOYSTVPMPTFGGKVEIKR 108
 Db 61 RFSGSGSGTDFLTITSLQPEDPATYTCQOYSTVPMPTFGGKVEIKR 108

RESULT 14

KVLA_HUMAN STANDARD; PRT; 108 AA.
 ID KVLA_HUMAN
 AC P01573;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-I region AG.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=69234734; PubMed=4893682;
 RA Tiltan K., Shinoda T., Putnam F.W.;
 RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
 RT complete sequence and the location of the disulfide bridges";
 RL J. Biol. Chem. 244:3550-3560(1969).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR, A01861; K1H0AG.
 DR HSSP, P01607; 1BMW.
 DR GO, GO:0005576; C:extracellular; NAS.
 DR GO, GO:0003823; P:antigen binding; NAS.
 DR GO, GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003586; IG-V.
 DR Pfam, PF00047; 1G, 1.
 DR SMART, SM00406; IGV, 1.
 DR PROSITE, PS50835; IG-LIKE; 1.
 KW Bence-Jones protein; Direct protein sequencing;
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DISULFID 98 107 Framework-4.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match 81.1%; Score 467; DB 1; Length 108;
 Best Local Similarity 82.4%; Pred. No. 2.8e-40;
 Matches 89; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITTCASQDISNLYNMYOQKPKAKYLYFTSSLHSGVPS 60
 Db 1 DIQMTQSPSSLSASVGDRTVITTCASQDISNLYNMYOQKPKAKYLYFTSSLHSGVPS 60
 61 RFSGSGSGTDFLTITSLQPEDPATYTCQOYSTVPMPTFGGKVEIKR 108
 Db 61 RFSGSGSGTDFLTITSLQPEDPATYTCQOYSTVPMPTFGGKVEIKR 108

RESULT 15

Qy 07Z473 PRELIMINARY; PRT; 234 AA.
 ID 07Z473;
 AC 07Z473;
 DT 01-OCT-2003 (TREMblrel. 25, Created)

```

DT 01-OCT-2003 (TRENBLrel. 25, last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=2238257; PubMed=1247732; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uadiri T.B., Toshlynski S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAH56256.1; -.
DR HSSP; P01834; IHEZ.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-bee; 1.
DR SMART; SM00406; Icy; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

```

Search completed: March 14, 2005, 20:49:18
 Job time : 77.193 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model1

Run on: March 14, 2005, 20:22:02 ; Search time 43.9912 Seconds
(without alignments)
884.760 Million cell updates/sec

Title: US-09-723-752b-7

Perfect score: 655
Sequence: 1 EVGLVSGGGLVPGGSLRL.....YPHYSSSHYFDWGGCTL 118

Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 1396920 seqs, 32984858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubppaa/PCRT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubppaa/PCRTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubppaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubppaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubppaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubppaa/US10E_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	655	100.0	118 9 US-09-056-1608-108	Sequence 108, App
2	655	100.0	118 14 US-10-234-671-7	Sequence 7, Appl
3	655	100.0	118 14 US-10-234-671-106	Sequence 106, App
4	655	100.0	118 15 US-10-624-153-96	Sequence 96, Appl
5	655	100.0	123 9 US-09-056-1608-7	Sequence 7, Appl
6	655	100.0	123 13 US-10-153-159-1	Sequence 1, Appl
7	655	100.0	123 13 US-10-153-159-14	Sequence 14, Appl
8	655	100.0	123 14 US-10-153-176-1	Sequence 14, Appl
9	655	100.0	123 14 US-10-153-176-14	Sequence 14, Appl
10	655	100.0	123 15 US-10-443-134A-1	Sequence 1, Appl
11	655	100.0	123 15 US-10-443-134A-14	Sequence 14, Appl
12	655	100.0	123 16 US-10-723-434-55	Sequence 55, Appl
13	655	100.0	123 17 US-10-877-532-8	Sequence 8, Appl

14	655	100.0	231 15 US-10-364-953-2	Sequence 2, Appl
15	651	99.4	118 9 US-09-056-1608-110	Sequence 110, App
16	651	99.4	118 14 US-10-234-671-108	Sequence 108, App
17	650	99.2	123 15 US-10-443-134A-126	Sequence 126, App
18	650	99.2	123 16 US-10-723-434-104	Sequence 129, App
19	649	99.1	123 15 US-10-443-134A-129	Sequence 129, App
20	649	99.1	123 16 US-10-723-434-170	Sequence 103, App
21	646	98.6	123 16 US-10-723-434-103	Sequence 59, App
22	645	98.5	123 16 US-10-723-434-59	Sequence 112, App
23	644	98.3	118 9 US-09-056-1608-112	Sequence 110, App
24	644	98.3	118 14 US-10-234-671-110	Sequence 97, App
25	644	98.3	118 15 US-10-624-153-97	Sequence 128, App
26	644	98.3	123 15 US-10-443-134A-128	Sequence 105, App
27	644	98.3	123 16 US-10-723-434-105	Sequence 105, App
28	644	98.3	231 15 US-10-364-953-5	Sequence 69, Appl
29	643	98.2	123 16 US-10-723-434-69	Sequence 69, Appl
30	642	98.0	118 9 US-09-056-1608-114	Sequence 114, App
31	642	98.0	118 14 US-10-234-671-112	Sequence 112, App
32	642	98.0	123 16 US-10-723-434-65	Sequence 65, Appl
33	638	97.4	9 US-09-056-1608-16	Sequence 16, Appl
34	638	97.4	123 14 US-10-234-671-16	Sequence 16, Appl
35	638	97.4	123 15 US-10-443-134A-130	Sequence 130, App
36	638	97.4	123 16 US-10-723-434-67	Sequence 67, App
37	638	97.4	123 16 US-10-723-434-101	Sequence 101, App
38	638	97.4	123 16 US-10-723-434-102	Sequence 102, App
39	638	97.4	231 15 US-10-364-953-9	Sequence 9, Appl
40	637	97.3	118 9 US-09-056-1608-106	Sequence 106, App
41	637	97.3	118 14 US-10-234-671-104	Sequence 104, App
42	636	97.1	123 15 US-10-443-134A-131	Sequence 131, App
43	636	97.1	123 16 US-10-723-434-77	Sequence 75, Appl
44	636	97.1	123 16 US-10-723-434-77	Sequence 77, Appl
45	636	97.1	123 16 US-10-723-434-84	Sequence 84, Appl

ALIGNMENTS

RESULT 1
US-09-056-1608-108
Sequence 108, Application US/090561608
Patent No. US2002003215A1
GENERAL INFORMATION:
APPLICANT: Beca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-Aug-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haack, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1039R2
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-1608-108

Query Match 100.0%; Score 655; DB 9; Length 118;
Best Local Similarity 100.0%; Pred. No. 2,1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGSLRLSCAAGYFTFTNYGMNWRQAPGKGLEWVGWINTYTGEPY 60
DB 1 EVOLVESGGGLVOPGSLRLSCAAGYFTFTNYGMNWRQAPGKGLEWVGWINTYTGEPY 60
QY 61 AADFKRRFTFSLDTSKSTAYLQNMNSLRADTAIVYCAKPHYGSSHWYFDVWGQTL 118
DB 61 AADFKRRFTFSLDTSKSTAYLQNMNSLRADTAIVYCAKPHYGSSHWYFDVWGQTL 118

RESULT 2

US-10-234-671-7
Sequence 7, Application US/10234671
Publication No. US20030190317A1

GENERAL INFORMATION:

APPLICANT: Baca, Manuel

Wells, James A.
Prestea, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.

TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpacin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/234,671

FILING DATE: 03-Sep-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/056160

FILING DATE: 06-APR-1998

APPLICATION NUMBER: 60/126446

FILING DATE: 07-APR-1997

APPLICATION NUMBER: 60/054856

FILING DATE: 06-AUG-1997

ATTORNEY/AGENT INFORMATION:

NAME: Cui, Steven X.

REGISTRATION NUMBER: 44,637

REFERENCE/DOCKET NUMBER: P1093R2C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 118 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-10-234-671-7
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
Query Match 100.0%; Score 655; DB 14; Length 118;

Best Local Similarity 100.0%; Pred. No. 2,1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGSLRLSCAAGYFTFTNYGMNWRQAPGKGLEWVGWINTYTGEPY 60
DB 1 EVOLVESGGGLVOPGSLRLSCAAGYFTFTNYGMNWRQAPGKGLEWVGWINTYTGEPY 60
QY 61 AADFKRRFTFSLDTSKSTAYLQNMNSLRADTAIVYCAKPHYGSSHWYFDVWGQTL 118
DB 61 AADFKRRFTFSLDTSKSTAYLQNMNSLRADTAIVYCAKPHYGSSHWYFDVWGQTL 118

RESULT 3

US-10-234-671-106
Sequence 106, Application US/10234671
Publication No. US20030190317A1

GENERAL INFORMATION:

APPLICANT: Baca, Manuel

Wells, James A.
Prestea, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.

TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpacin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/234,671

FILING DATE: 03-Sep-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/056160

FILING DATE: 06-APR-1998

APPLICATION NUMBER: 60/126446

FILING DATE: 07-APR-1997

APPLICATION NUMBER: 60/054856

FILING DATE: 06-AUG-1997

ATTORNEY/AGENT INFORMATION:

NAME: Cui, Steven X.

REGISTRATION NUMBER: 44,637

REFERENCE/DOCKET NUMBER: P1093R2C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 106:

SEQUENCE CHARACTERISTICS:

LENGTH: 118 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 106:

US-10-234-671-106
Query Match 100.0%; Score 655; DB 14; Length 118;
Best Local Similarity 100.0%; Pred. No. 2,1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGSLRLSCAAGYFTFTNYGMNWRQAPGKGLEWVGWINTYTGEPY 60
DB 1 EVOLVESGGGLVOPGSLRLSCAAGYFTFTNYGMNWRQAPGKGLEWVGWINTYTGEPY 60
QY 61 AADFKRRFTFSLDTSKSTAYLQNMNSLRADTAIVYCAKPHYGSSHWYFDVWGQTL 118
DB 61 AADFKRRFTFSLDTSKSTAYLQNMNSLRADTAIVYCAKPHYGSSHWYFDVWGQTL 118

RESULT 4
US-10-624-153-96
Sequence 96, Application US/10624153
Publication No. US20040086502A1
GENERAL INFORMATION:
APPLICANT: CHEN, YVONNE M.
APPLICANT: LOWMAN, HENRY B.
APPLICANT: MULLER, YVES
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1C
CURRENT APPLICATION NUMBER: US/10/624,153
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: US 09/440,781
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: US 60/108,945
PRIOR FILING DATE: 1998-11-18
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 96
LENGTH: 118
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
NAME/KEY: artificial
LOCATION: 1-118
OTHER INFORMATION: humanized antibody heavy chain variable domain
US-10-624-153-96

Query Match 100.0%; Score 655; DB 15; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVOLVESGGGLVQPGGSLRLSCAASGTTFTYGMNWVROAPGKGLEWVGWINTYTGPPT 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGTTFTYGMNWVROAPGKGLEWVGWINTYTGPPT 60
QY 61 AADFKRRFTPSLDTSKSTAYLQWNSLRADTAAYYCAKPHYYGSSHWYFDVWGQGL 118
DB 61 AADFKRRFTPSLDTSKSTAYLQWNSLRADTAAYYCAKPHYYGSSHWYFDVWGQGL 118

RESULT 5
US-09-056-160B-7
Sequence 7, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, Manuel A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-7

Query Match 100.0%; Score 655; DB 9; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVOLVESGGGLVQPGGSLRLSCAASGTTFTYGMNWVROAPGKGLEWVGWINTYTGPPT 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGTTFTYGMNWVROAPGKGLEWVGWINTYTGPPT 60
QY 61 AADFKRRFTPSLDTSKSTAYLQWNSLRADTAAYYCAKPHYYGSSHWYFDVWGQGL 118
DB 61 AADFKRRFTPSLDTSKSTAYLQWNSLRADTAAYYCAKPHYYGSSHWYFDVWGQGL 118

RESULT 6
US-10-153-159-1
Sequence 1, Application US/10153159
Publication No. US20020177170A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
APPLICANT: Helel, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Caili
TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY LIE
FILE REFERENCE: 26050-704
CURRENT APPLICATION NUMBER: US/10/153,159
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH of parental anti-VEGF antibody
US-10-153-159-1

Query Match 100.0%; Score 655; DB 13; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVOLVESGGGLVQPGGSLRLSCAASGTTFTYGMNWVROAPGKGLEWVGWINTYTGPPT 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGTTFTYGMNWVROAPGKGLEWVGWINTYTGPPT 60
QY 61 AADFKRRFTPSLDTSKSTAYLQWNSLRADTAAYYCAKPHYYGSSHWYFDVWGQGL 118
DB 61 AADFKRRFTPSLDTSKSTAYLQWNSLRADTAAYYCAKPHYYGSSHWYFDVWGQGL 118

RESULT 7
US-10-153-159-14
Sequence 14, Application US/10153159

```
Publication No. US20020177170A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
APPLICANT: Heien, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Calli
TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY LIB
FILE REFERENCE: 26050-704
CURRENT APPLICATION NUMBER: US/10/153,159
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH of AM2-ccFv
US-10-153-159-14

Query Match      100.0%; Score 655; DB 13; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVPGGSLRLSCAASGTTFTNYGMNWRQAPGKGLEWVGWINTYTGEPT 60
DB 1 EVOLVESGGGLVPGGSLRLSCAASGTTFTNYGMNWRQAPGKGLEWVGWINTYTGEPT 60
QY 61 AADFKRRFTSLDTSKSTAYLQNSLRADTAIVYCAKPHYGSSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQNSLRADTAIVYCAKPHYGSSHWYFDVWGQGL 118

RESULT 8
US-10-153-176-1
Sequence 1, Application US/10153176
Publication No. US20030022240A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
APPLICANT: Heien, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Calli
APPLICANT: Cao, Yicheng
APPLICANT: Li, Shengfeng
APPLICANT: Liu, Shengjiang
TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO
FILE REFERENCE: 26050-701
CURRENT APPLICATION NUMBER: US/10/153,176
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH of parental anti-VEGF antibody
US-10-153-176-1

Query Match      100.0%; Score 655; DB 14; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVPGGSLRLSCAASGTTFTNYGMNWRQAPGKGLEWVGWINTYTGEPT 60
DB 1 EVOLVESGGGLVPGGSLRLSCAASGTTFTNYGMNWRQAPGKGLEWVGWINTYTGEPT 60
QY 61 AADFKRRFTSLDTSKSTAYLQNSLRADTAIVYCAKPHYGSSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQNSLRADTAIVYCAKPHYGSSHWYFDVWGQGL 118

RESULT 9
US-10-153-176-14
Sequence 14, Application US/10153176
Publication No. US20030022240A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
APPLICANT: Heien, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Calli
APPLICANT: Cao, Yicheng
APPLICANT: Li, Shengfeng
APPLICANT: Liu, Shengjiang
TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO
FILE REFERENCE: 26050-701
CURRENT APPLICATION NUMBER: US/10/153,176
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH of AM2-ccFv
US-10-153-176-14

Query Match      100.0%; Score 655; DB 14; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVPGGSLRLSCAASGTTFTNYGMNWRQAPGKGLEWVGWINTYTGEPT 60
DB 1 EVOLVESGGGLVPGGSLRLSCAASGTTFTNYGMNWRQAPGKGLEWVGWINTYTGEPT 60
QY 61 AADFKRRFTSLDTSKSTAYLQNSLRADTAIVYCAKPHYGSSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQNSLRADTAIVYCAKPHYGSSHWYFDVWGQGL 118

RESULT 10
US-10-443-134A-1
Sequence 1, Application US/10443134A
Publication No. US20040010376A1
GENERAL INFORMATION:
APPLICANT: Luo, Peizhi
APPLICANT: Heien, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Calli
APPLICANT: Cao, Yicheng
APPLICANT: Li, Shengfeng
APPLICANT: Liu, Shengjiang
TITLE OF INVENTION: GENERATION AND SELECTION OF PROTEIN LIBRARY IN SILICO
FILE REFERENCE: 26050-709
CURRENT APPLICATION NUMBER: US/10/443,134A
CURRENT FILING DATE: 2003-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: US 10/153,176
PRIOR FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/153,159
```

```
DB 1 EVOLVESGGGLVPGGSLRLSCAASGTTFTNYGMNWRQAPGKGLEWVGWINTYTGEPT 60
QY 61 AADFKRRFTSLDTSKSTAYLQNSLRADTAIVYCAKPHYGSSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQNSLRADTAIVYCAKPHYGSSHWYFDVWGQGL 118

RESULT 9
US-10-153-176-14
Sequence 14, Application US/10153176
Publication No. US20030022240A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
APPLICANT: Heien, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Calli
APPLICANT: Cao, Yicheng
APPLICANT: Li, Shengfeng
APPLICANT: Liu, Shengjiang
TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO
FILE REFERENCE: 26050-701
CURRENT APPLICATION NUMBER: US/10/153,176
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH of AM2-ccFv
US-10-153-176-14

Query Match      100.0%; Score 655; DB 14; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVPGGSLRLSCAASGTTFTNYGMNWRQAPGKGLEWVGWINTYTGEPT 60
DB 1 EVOLVESGGGLVPGGSLRLSCAASGTTFTNYGMNWRQAPGKGLEWVGWINTYTGEPT 60
QY 61 AADFKRRFTSLDTSKSTAYLQNSLRADTAIVYCAKPHYGSSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQNSLRADTAIVYCAKPHYGSSHWYFDVWGQGL 118

RESULT 10
US-10-443-134A-1
Sequence 1, Application US/10443134A
Publication No. US20040010376A1
GENERAL INFORMATION:
APPLICANT: Luo, Peizhi
APPLICANT: Heien, Mark
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Calli
APPLICANT: Cao, Yicheng
APPLICANT: Li, Shengfeng
APPLICANT: Liu, Shengjiang
TITLE OF INVENTION: GENERATION AND SELECTION OF PROTEIN LIBRARY IN SILICO
FILE REFERENCE: 26050-709
CURRENT APPLICATION NUMBER: US/10/443,134A
CURRENT FILING DATE: 2003-05-20
PRIOR APPLICATION NUMBER: US 10/125,687
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/284,407
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: US 10/153,176
PRIOR FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/153,159
```


;; PRIOR FILING DATE: 2002-05-20
;; NUMBER OF SEQ ID NOS: 131
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 1
;; LENGTH: 123
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: VH of parental anti-VEGF antibody
US-10-443-134A-1

Query Match 100.0%; Score 655; DB 15; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGTTFTNYGMNWRQAPGKLEWVGINTYTGEPY 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGTTFTNYGMNWRQAPGKLEWVGINTYTGEPY 60
QY 61 AADPKRFTFSLDTSKSTAYLQWNSLRADTAIVYCAKPHYGSSHWYFDVWGQGL 118
DB 61 AADPKRFTFSLDTSKSTAYLQWNSLRADTAIVYCAKPHYGSSHWYFDVWGQGL 118

RESULT 11
US-10-443-134A-14
;; Sequence 14, Application US/10443134A
;; Publication No. US20040010376A1
;; GENERAL INFORMATION:
;; APPLICANT: Lnc, Peizhi
;; APPLICANT: Heieh, Mark
;; APPLICANT: Zhong, Pingyu
;; APPLICANT: Wang, Caoli
;; APPLICANT: Cao, Yicheng
;; APPLICANT: Liu, Shengjiang
;; TITLE OF INVENTION: GENERATION AND SELECTION OF PROTEIN LIBRARY IN SILICO
;; FILE REFERENCE: 26050-709
;; CURRENT APPLICATION NUMBER: US/10/443,134A
;; PRIOR FILING DATE: 2003-05-20
;; PRIOR APPLICATION NUMBER: US 10/125,687
;; PRIOR FILING DATE: 2002-04-17
;; PRIOR APPLICATION NUMBER: US 60/284,407
;; PRIOR FILING DATE: 2001-04-17
;; PRIOR APPLICATION NUMBER: US 10/153,176
;; PRIOR FILING DATE: 2002-05-20
;; PRIOR APPLICATION NUMBER: US 10/153,159
;; PRIOR FILING DATE: 2002-05-20
;; NUMBER OF SEQ ID NOS: 131
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 14
;; LENGTH: 123
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: VH of AM2-ccFv
US-10-443-134A-14

Query Match 100.0%; Score 655; DB 15; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGTTFTNYGMNWRQAPGKLEWVGINTYTGEPY 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGTTFTNYGMNWRQAPGKLEWVGINTYTGEPY 60
QY 61 AADPKRFTFSLDTSKSTAYLQWNSLRADTAIVYCAKPHYGSSHWYFDVWGQGL 118
DB 61 AADPKRFTFSLDTSKSTAYLQWNSLRADTAIVYCAKPHYGSSHWYFDVWGQGL 118

RESULT 12
US-10-723-434-55
;; Sequence 55, Application US/10723434

;; Publication No. US20040133357A1
;; GENERAL INFORMATION:
;; APPLICANT: Zhong, Pingyu
;; APPLICANT: Luo, Peizhi
;; APPLICANT: Wang, Kevin C.
;; APPLICANT: Heieh, Mark
;; APPLICANT: Li, Yan
;; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
;; FILE REFERENCE: 26050-709.501
;; CURRENT APPLICATION NUMBER: US/10/723,434
;; PRIOR FILING DATE: 2003-11-26
;; PRIOR APPLICATION NUMBER: US 60/284,407
;; PRIOR FILING DATE: 2001-04-17
;; PRIOR APPLICATION NUMBER: US 10/125,687
;; PRIOR FILING DATE: 2002-04-17
;; PRIOR APPLICATION NUMBER: US 10/153,176
;; PRIOR FILING DATE: 2002-05-20
;; PRIOR APPLICATION NUMBER: US 10/443,134
;; PRIOR FILING DATE: 2003-05-20
;; NUMBER OF SEQ ID NOS: 156
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 55
;; LENGTH: 123
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: VH
US-10-723-434-55

Query Match 100.0%; Score 655; DB 16; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGTTFTNYGMNWRQAPGKLEWVGINTYTGEPY 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGTTFTNYGMNWRQAPGKLEWVGINTYTGEPY 60
QY 61 AADPKRFTFSLDTSKSTAYLQWNSLRADTAIVYCAKPHYGSSHWYFDVWGQGL 118
DB 61 AADPKRFTFSLDTSKSTAYLQWNSLRADTAIVYCAKPHYGSSHWYFDVWGQGL 118

RESULT 13
US-10-877-532-8
;; Sequence 8, Application US/10877532
;; Publication No. US20050038231A1
;; GENERAL INFORMATION:
;; APPLICANT: FAHRNER, ROBERT L.
;; APPLICANT: LAVERDIERE, AMY
;; APPLICANT: MCDONALD, PAUL J.
;; APPLICANT: O'LEARY, RHONA M.
;; TITLE OF INVENTION: REDUCING PROTEIN A LEACHING DURING PROTEIN A AFFINITY CHROMATOGR
;; FILE REFERENCE: P2015R1
;; CURRENT APPLICATION NUMBER: US/10/877,532
;; PRIOR FILING DATE: 2004-06-24
;; PRIOR APPLICATION NUMBER: US 60/490,500
;; PRIOR FILING DATE: 2003-07-28
;; NUMBER OF SEQ ID NOS: 8
;; SEQ ID NO 8
;; LENGTH: 123
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: sequence is synthesized
US-10-877-532-8

Query Match 100.0%; Score 655; DB 17; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGTTFTNYGMNWRQAPGKLEWVGINTYTGEPY 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGTTFTNYGMNWRQAPGKLEWVGINTYTGEPY 60

QY 61 AADFKRRFTSLDTSKSTAYLQNNSLRAEDTAVYYCAKPHYGSSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQNNSLRAEDTAVYYCAKPHYGSSHWYFDVWGQGL 118

RESULT 14

US-10-364-953-2
Sequence 2, Application US/10364953
Publication No. US20030224397A1
GENERAL INFORMATION:
APPLICANT: LOWMAN, HENRY B.
APPLICANT: MARVIN, JONATHAN S.
TITLE OF INVENTION: ANTIBODY VARIANTS WITH PASTER ANTIGEN ASSOCIATION RATES
FILE REFERENCE: P1951R1
CURRENT APPLICATION NUMBER: US/10/364,953
CURRENT FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US 60/355,895
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/409,685
PRIOR FILING DATE: 2002-09-10
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 2
LENGTH: 231
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: Artificial Sequence
LOCATION: Full
OTHER INFORMATION: Y0101-VH
US-10-364-953-2

Query Match 100.0%; Score 655; DB 15; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.8e-47;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGSLRLSCAASGFTFTNGMNVRQAPGKLEWVGWINTYTGEPT 60
DB 1 EVOLVESGGGLVQPGSLRLSCAASGFTFTNGMNVRQAPGKLEWVGWINTYTGEPT 60
QY 61 AADFKRRFTSLDTSKSTAYLQNNSLRAEDTAVYYCAKPHYGSSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQNNSLRAEDTAVYYCAKPHYGSSHWYFDVWGQGL 118

RESULT 15

US-09-056-160B-110
Sequence 110, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-110

Query Match 99.4%; Score 651; DB 9; Length 118;
Best Local Similarity 99.2%; Pred. No. 4.4e-47;
Matches 117; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGSLRLSCAASGFTFTNGMNVRQAPGKLEWVGWINTYTGEPT 60
DB 1 EVOLVESGGGLVQPGSLRLSCAASGFTFTNGMNVRQAPGKLEWVGWINTYTGEPT 60
QY 61 AADFKRRFTSLDTSKSTAYLQNNSLRAEDTAVYYCAKPHYGSSHWYFDVWGQGL 118
DB 61 AADFKRRFTSLDTSKSTAYLQNNSLRAEDTAVYYCAKPHYGSSHWYFDVWGQGL 118

Search completed: March 14, 2005, 20:42:11
Job time : 44.9912 sec

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OW protein - protein search, using sw model

Run on: March 14, 2005, 20:30:13, Search time 24.3246 Seconds
(without alignments)
362.127 Million cell updates/sec

Title: US-09-723-752b-7

Perfect score: 655

Sequence: 1 EVOLVESGGGLVOPGSLRL.....YPHYSSGSHWYFDVWGQCTL 118

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: Issued Patents AA: *
2: /cgn2_6/ptodata/1/1aa/5A_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	655	100.0	118	4	US-09-440-781-96
2	644	98.3	118	4	US-09-440-781-97
3	631.5	96.4	121	4	US-09-440-781-98
4	631	96.3	491	4	US-10-011-125A-2
5	620.5	94.7	121	4	US-09-440-781-99
6	513.5	78.4	118	1	US-08-425-336-126
7	513.5	78.4	118	1	US-08-488-113B-126
8	513.5	78.4	118	1	US-08-477-484B-126
9	513.5	78.4	118	2	US-08-646-360-126
10	513.5	78.4	118	3	US-08-839-765-126
11	513.5	78.4	118	3	US-09-136-389-126
12	513.5	78.4	118	3	US-09-610-838-126
13	513.5	78.4	118	4	US-09-711-485-126
14	513.5	78.4	240	1	US-08-488-113B-147
15	513.5	78.4	240	1	US-08-488-113B-148
16	513.5	78.4	240	1	US-08-477-484B-147
17	513.5	78.4	240	1	US-08-477-484B-148
18	513.5	78.4	240	2	US-08-646-360-147
19	513.5	78.4	240	2	US-08-646-360-148
20	513.5	78.4	240	3	US-08-839-765-147
21	513.5	78.4	240	3	US-08-839-765-148
22	513.5	78.4	240	3	US-09-136-389-147
23	513.5	78.4	240	3	US-09-136-389-148
24	513.5	78.4	240	3	US-09-610-838-147
25	513.5	78.4	240	3	US-09-610-838-148
26	513.5	78.4	240	4	US-09-711-485-147
27	513.5	78.4	240	4	US-09-711-485-148

28	499.5	76.3	118	1	US-08-107-669D-29	Sequence 29, Appl
29	499.5	76.3	118	1	US-08-472-768A-29	Sequence 29, Appl
30	499.5	76.3	118	2	US-08-477-531B-29	Sequence 29, Appl
31	499.5	76.3	118	2	US-08-082-842A-29	Sequence 29, Appl
32	498.5	76.1	118	1	US-08-107-669D-67	Sequence 67, Appl
33	498.5	76.1	118	1	US-08-472-768A-89	Sequence 89, Appl
34	498.5	76.1	118	2	US-08-477-531B-67	Sequence 67, Appl
35	498.5	76.1	118	2	US-08-082-842A-89	Sequence 89, Appl
36	496.5	75.8	122	2	US-07-934-373C-20	Sequence 20, Appl
37	496.5	75.8	122	3	US-08-437-642B-20	Sequence 20, Appl
38	496.5	75.8	122	4	US-08-146-206C-20	Sequence 20, Appl
39	496.5	75.8	122	4	US-09-705-686-20	Sequence 20, Appl
40	496.5	75.8	122	4	US-09-705-392A-20	Sequence 20, Appl
41	496.5	75.8	122	4	US-09-705-398-20	Sequence 20, Appl
42	496.5	75.8	122	5	PCT-US93-07832-20	Sequence 20, Appl
43	495.5	75.6	122	2	US-07-934-373C-45	Sequence 45, Appl
44	495.5	75.6	122	3	US-08-437-642B-45	Sequence 45, Appl
45	495.5	75.6	122	4	US-08-146-206C-26	Sequence 26, Appl

ALIGNMENTS

```
RESULT 1
US-09-440-781-96
Sequence 96, Application US/09440781
Patent No. 6632926
GENERAL INFORMATION:
APPLICANT: Yvonne Man-Yee Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 96
LENGTH: 118
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-118
OTHER INFORMATION: humanized antibody heavy chain variable domain
US-09-440-781-96

Query Match      100.0%; Score 655; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 3.2e-59;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 EVOLVESGGGLVOPGSLRLSCAASGFTFTYGMNWVROAPGKLEWGWINTYGEPT 60
Db 1 EVOLVESGGGLVOPGSLRLSCAASGFTFTYGMNWVROAPGKLEWGWINTYGEPT 60
Cy 61 AADPKRRFTFLDPSKSTAYLQNNSLRAEDTAVYYCAKPHYYSGSHWYFDVWGQCTL 118
Db 61 AADPKRRFTFLDPSKSTAYLQNNSLRAEDTAVYYCAKPHYYSGSHWYFDVWGQCTL 118

RESULT 2
US-09-440-781-97
Sequence 97, Application US/09440781
Patent No. 6632926
GENERAL INFORMATION:
APPLICANT: Yvonne Man-Yee Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 97
LENGTH: 118
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
```

NAME/KEY: artificial
LOCATION: 1-118
OTHER INFORMATION: humanized antibody heavy chain variable domain
US-09-440-781-97

Query Match 98.3%; Score 644; DB 4; Length 118;
Best Local Similarity 98.3%; Pred. No. 4.2e-58;
Matches 116; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYFTNYGMNVRQAPGKLEWGMINTYGEPT 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGYDFTNYGMNVRQAPGKLEWGMINTYGEPT 60

QY 61 AADFRRTFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQGT 118
DB 61 AADFRRTFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQGT 118

RESULT 3
US-09-440-781-98
Sequence 98, Application US/09440781
Patent No. 6632926

GENERAL INFORMATION:
APPLICANT: Yvonne Man-yea Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99

SEQ ID NO 98
LENGTH: 121
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-121
OTHER INFORMATION: humanized antibody heavy chain variable domain
US-09-440-781-98

Query Match 96.4%; Score 631.5; DB 4; Length 121;
Best Local Similarity 95.9%; Pred. No. 8e-57;
Matches 116; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYFTNYGMNVRQAPGKLEWGMINTYGEPT 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGYFTNYGMNVRQAPGKLEWGMINTYGEPT 60

QY 61 AADFRRTFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHY--GSSHWYFDVWGQGT 117
DB 61 AADFRRTFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYVNERKSHWYFDVWGQGT 120

QY 118 L 118
DB 121 L 121

RESULT 4
US-10-011-125A-2
Sequence 2, Application US/10011125A
Patent No. 6828121

GENERAL INFORMATION:
APPLICANT: Chen, Christena Yu-Ching
TITLE OF INVENTION: BACTERIAL HOST STRAINS
FILE REFERENCE: P1804R1
CURRENT APPLICATION NUMBER: US/10/011,125A
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 12

SEQ ID NO 2
LENGTH: 491
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Sequence is synthesized.
Patent No. 6828121
US-10-011-125A-2

Query Match 96.3%; Score 631; DB 4; Length 491;
Best Local Similarity 94.9%; Pred. No. 4.7e-56;
Matches 112; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYFTNYGMNVRQAPGKLEWGMINTYGEPT 60
DB 261 EVOLVESGGGLVQPGGSLRLSCAASGYFTNYGMNVRQAPGKLEWGMINTYGEPT 320

QY 61 AADFRRTFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQGT 118
DB 321 AADFRRTFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQGT 378

RESULT 5
US-09-440-781-99
Sequence 99, Application US/09440781
Patent No. 6632926

GENERAL INFORMATION:
APPLICANT: Yvonne Man-yea Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99

SEQ ID NO 99
LENGTH: 121
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-121
OTHER INFORMATION: humanized antibody heavy chain variable domain
US-09-440-781-99

Query Match 94.7%; Score 620.5; DB 4; Length 121;
Best Local Similarity 94.2%; Pred. No. 1e-55;
Matches 114; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYFTNYGMNVRQAPGKLEWGMINTYGEPT 60
DB 1 EVOLVESGGGLVQPGGSLRLSCAASGYDFTNYGMNVRQAPGKLEWGMINTYGEPT 60

QY 61 AADFRRTFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHY--GSSHWYFDVWGQGT 117
DB 61 AADFRRTFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYVNERKSHWYFDVWGQGT 120

QY 118 L 118
DB 121 L 121

RESULT 6
US-08-425-336-126
Sequence 126, Application US/08425336
Patent No. 5621083

GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studilka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESSES:
ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA

LENGTH: 1111
TYPE: PRT
COUNTRY: USA

ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 31194
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-425-336-126

Query Match 78.4%; Score 513.5; DB 1; Length 118;
Best Local Similarity 78.6%; Pred. No. 7.5e-45;
Matches 92; Conservative 12; Mismatches 8; Indels 5; Gaps 1;
QY 1 EVLVESGGGLVOPGSLRLSCAASGTFRTNYGMNWVRQAPGKGLIEWGMINTYGEPTY 60
DB 1 EIQLVQSGGLVKKPGSVRISCAASGYFTFTNYGMNWVRQAPGKGLIEWGMINTYGEPTY 60
QY 61 AADFRRTFSLDPSKNTAVYQINSLRADTAIVYCAKPHYSGSHYFDVWGCGT 117
DB 61 ADFRGRFTFSLDPSKNTAVYQINSLRADTAIVYFCTIRGY----DWYFDVWGCGT 112

RESULT 7
US-08-488-113B-126
Sequence 126, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B

FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-113B-126

Query Match 78.4%; Score 513.5; DB 1; Length 118;
Best Local Similarity 78.6%; Pred. No. 7.5e-45;
Matches 92; Conservative 12; Mismatches 8; Indels 5; Gaps 1;
QY 1 EVLVESGGGLVOPGSLRLSCAASGTFRTNYGMNWVRQAPGKGLIEWGMINTYGEPTY 60
DB 1 EIQLVQSGGLVKKPGSVRISCAASGYFTFTNYGMNWVRQAPGKGLIEWGMINTYGEPTY 60
QY 61 AADFRRTFSLDPSKNTAVYQINSLRADTAIVYCAKPHYSGSHYFDVWGCGT 117
DB 61 ADFRGRFTFSLDPSKNTAVYQINSLRADTAIVYFCTIRGY----DWYFDVWGCGT 112

RESULT 8
US-08-477-484B-126
Sequence 126, Application US/08477484B
Patent No. 5756699
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995

```
;
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-477-484B-126

Query Match 78.4%; Score 513.5; DB 1; Length 118;
Best Local Similarity 78.6%; Pred. No. 7.5e-45;
Matches 92; Conservative 12; Mismatches 8; Indels 5; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNGMNWVRQAPGKGLVWGINTYTGSPY 60
Db 1 EIQLVQSGGGLVQPGGSVRISCAASGYTFITNGMNWVRQAPGKGLVWGINTYTGSPY 60

Qy 61 AADPKRPTFLSDTSKSTAYLQMSLRADETAVYCAKPHYGGSSHWYFDVWGQGT 117
Db 61 ADSPKGRPTFLSDSKNTAYLQINSRAEDTAVYFCTRRGY-----DWYFDVWGQGT 112

RESULT 9
US-08-646-360-126
; Sequence 126, Application US/08646360
; Patent No. 5837491
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
```

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-646-360-126

Query Match 78.4%; Score 513.5; DB 2; Length 118;
Best Local Similarity 78.6%; Pred. No. 7.5e-45;
Matches 92; Conservative 12; Mismatches 8; Indels 5; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNGMNWVRQAPGKGLVWGINTYTGSPY 60
Db 1 EIQLVQSGGGLVQPGGSVRISCAASGYTFITNGMNWVRQAPGKGLVWGINTYTGSPY 60

Qy 61 AADPKRPTFLSDTSKSTAYLQMSLRADETAVYCAKPHYGGSSHWYFDVWGQGT 117
Db 61 ADSPKGRPTFLSDSKNTAYLQINSRAEDTAVYFCTRRGY-----DWYFDVWGQGT 112

RESULT 10
US-08-839-765-126
; Sequence 126, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
```

RESULT 11
US-09-136-389-126
; Sequence 126, Application US/091136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/646,360

```

RESULT 12
US-09-610-838-126
; Sequence 126, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: US 09/136,389
FILING DATE: 18-AUG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70-P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9155
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-610-838-126

Query Match 78.4%; Score 513.5; DB 3; Length 118;
Best Local Similarity 78.6%; Pred. No. 7.5e-45;
Matches 92; Conservative 12; Mismatches 8; Indels 5; Gaps 1;

QY 1 EVOLVESGGLVOPGGSRLSLSCAASGYFTNYGMNVVRQAPGKLEWGVNHTYGTPT 60
DB 1 EIQLVQSGGLVKGPGSVRISCAASGYFTNYGMNVVRQAPGKLEWGVNHTYGTPT 60
QY 61 AADFKRFTSLDTSKSTAYLQNSLRADTAVYCYCAKYPHYGSSHWYFDVWGQGT 117
DB 61 ADSFKGRFTSLDSDSKNTAYLQNSLRADTAVYCTTRGY-----DWYFDVWGQGT 112

RESULT 13
US-09-711-485-126
Sequence 126, Application US/09711485
Patent No. 6649742
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/711,485

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/839,765
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70-P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9155
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-711-485-126

Query Match 78.4%; Score 513.5; DB 4; Length 118;
Best Local Similarity 78.6%; Pred. No. 7.5e-45;
Matches 92; Conservative 12; Mismatches 8; Indels 5; Gaps 1;

QY 1 EVOLVESGGLVOPGGSRLSLSCAASGYFTNYGMNVVRQAPGKLEWGVNHTYGTPT 60
DB 1 EIQLVQSGGLVKGPGSVRISCAASGYFTNYGMNVVRQAPGKLEWGVNHTYGTPT 60
QY 61 AADFKRFTSLDTSKSTAYLQNSLRADTAVYCYCAKYPHYGSSHWYFDVWGQGT 117
DB 61 ADSFKGRFTSLDSDSKNTAYLQNSLRADTAVYCTTRGY-----DWYFDVWGQGT 112

RESULT 14
US-08-488-113B-147
Sequence 147, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995


```

; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 147:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-113B-147

```

```

Query Match      78.4%; Score 513.5; DB 1; Length 240;
Best Local Similarity 78.6%; Pred. No. 1.7e-44;
Matches 92; Conservative 12; Mismatches 8; Indels 5; Gaps 1;

Qy 1 EVLVESGGGLVOPGGSLRLSCAASGYTFTNYGMNVRQAPGKGLWVGWINTYTGPTY 60
Db 123 EIQLVQSGGGLVPGGSLRLSCAASGYTFTNYGMNVRQAPGKGLWVGWINTYTGPTY 182
Qy 61 AADPKRFTSLDTSKSTAYLQNSLRADTAIVYCAKYPHYGSSHWYFDVWGQGT 117
Db 183 ADSFKGRFTSLDSDSKNTAYLQNSLRADTAIVYCAKYPHYGSSHWYFDVWGQGT 234

```

RESULT 15

```

US-08-488-113B-148
; Sequence 148, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:

```

```

; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-113B-148

```

```

Query Match      78.4%; Score 513.5; DB 1; Length 240;
Best Local Similarity 78.6%; Pred. No. 1.7e-44;
Matches 92; Conservative 12; Mismatches 8; Indels 5; Gaps 1;

Qy 1 EVLVESGGGLVOPGGSLRLSCAASGYTFTNYGMNVRQAPGKGLWVGWINTYTGPTY 60
Db 1 EIQLVQSGGGLVPGGSLRLSCAASGYTFTNYGMNVRQAPGKGLWVGWINTYTGPTY 60
Qy 61 AADPKRFTSLDTSKSTAYLQNSLRADTAIVYCAKYPHYGSSHWYFDVWGQGT 117
Db 61 ADSFKGRFTSLDSDSKNTAYLQNSLRADTAIVYCAKYPHYGSSHWYFDVWGQGT 112

```

Search completed: March 14, 2005, 20:43:51
Job time : 25.3246 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2005, 20:21:17 ; Search time 94.4518 Seconds
(without alignments)
483.186 Million cell updates/sec

Title: US-09-723-752B-7
Perfect score: 655
Sequence: 1 EVQLVDSGGGLVQPGGSLRL.....YPHYGSHWFDVWGQSTL 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003s:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	655	100.0	118	2	Aaw70678
2	655	100.0	118	3	AAB05899
3	655	100.0	118	3	AAB13381
4	655	100.0	118	3	AAB13389
5	655	100.0	118	5	ABP61247
6	655	100.0	123	2	Aaw70617
7	655	100.0	123	5	ABP61186
8	655	100.0	123	8	ADG31767
9	655	100.0	123	8	ADG31780
10	655	100.0	231	7	ADC26155
11	655	100.0	476	8	ADQ90736
12	651	99.4	118	2	Aaw70680
13	651	99.4	118	5	ABP61249
14	650	99.2	123	8	ADG31892
15	649	99.1	123	8	ADG31895
16	644	98.3	118	2	Aaw70682
17	644	98.3	118	3	AAB05900
18	644	98.3	118	3	AAB13382
19	644	98.3	118	5	ABP61251
20	644	98.3	123	8	ADG31894
21	644	98.3	231	7	ADC26158
22	642	98.0	118	2	Aaw70684
23	642	98.0	118	3	AAB13383
24	642	98.0	118	5	ABP61253
25	638	97.4	123	2	Aaw70626

ALIGNMENTS

RESULT 1

AAW70678
ID AAW70678 standard; peptide; 118 AA.
AC AAW70678;
XX
DT 27-JAN-1999 (first entry)
DS Anti-VEGF humanised antibody variable heavy domain of variant Y0101.
XX Heavy variable domain; murine; humanised antibody;
KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
KW VEGF-induced angiogenesis; tumour; retinal disorder;
KW age-related macular degeneration; diabetic retinopathy;
KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
XX Synthetic.
OS Mus sp.
OS Homo sapiens.
PN WO9845331-A2.
XX
PD 15-OCT-1998.
XX
XX 03-APR-1998; 98WO-US006604.
PR 07-APR-1997; 97US-00833504.
XX 06-AUG-1997; 97US-00908469.
XX (GETH) GENENTECH INC.
XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
XX WPI; 1998-568337/48.
XX New humanised antibody with affinity for vascular endothelial growth factor - for treatment of tumours, retinal disease and other angiogenic states, also related nucleic acid, vectors and transformed cells.
XX Example 3; Fig 9B; 100pp; English.

The present sequence represents a variable heavy domain of an affinity-matured anti-vascular endothelial growth factor (anti-VEGF) antibody variant. The sequence is used in the course of the invention to produce the humanised anti-VEGF antibody of the invention. The humanised antibodies are used to inhibit VEGF-induced angiogenesis, particularly for treating or preventing tumours (of any type) and retinal disorders (e.g. age-related macular degeneration or diabetic retinopathy). They can

CC also be used to treat other conditions that involve angiogenesis, e.g.
 CC rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc

XX SQ Sequence 118 AA;
 Query Match 100.0%; Score 655; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 4.5e-55;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNGMNWVRQAPGKLEWVGWINTYTGSPY 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNGMNWVRQAPGKLEWVGWINTYTGSPY 60
 QY 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQGTLL 118
 DB 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQGTLL 118

RESULT 2
 AAB05899
 ID AAB05899 standard; peptide; 118 AA.
 XX
 AC AAB05899;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Humanised anti-VEGF antibody F(ab)-12 heavy chain variable domain.
 XX
 KW Humanised; F(ab)-12; heavy chain variable domain; antibody variant;
 KW phage display; randomised library; cytostatic; antiarthritic;
 KW antipruritic; antidiabetic; antiinflammatory; antiarteriosclerotic;
 KW vascular endothelial growth factor; VEGF; breast cancer; lung cancer;
 KW retinoblastoma; rheumatoid arthritis; psoriasis; atherosclerosis;
 KW diabetic retinopathy; complementarity determining region; CDR.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200029584-A1.
 XX
 PD 25-MAY-2000.
 XX
 PF 16-NOV-1999; 99WO-US027153.
 XX
 PR 18-NOV-1998; 98US-0108945P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Chen YM, Lowman HB, Muller Y;
 XX
 DR WPI; 2000-387797/33.
 XX
 PT Antibody variants with higher binding affinity than native antibodies
 PT useful for diagnosis, prevention and treatment of neoplastic and non-
 PT neoplastic diseases comprises amino acid insertion in hypervariable
 FT region.
 XX
 PS Disclosure; Fig 1B; 110pp; English.
 XX

CC The present sequence is the heavy chain variable domain of F(ab)-12, a
 CC humanised anti-vascular endothelial growth factor (VEGF) antibody. F(ab)-
 CC 12 was the parent antibody used in the production of a large number of
 CC antibody variants containing randomised peptide inserts within the
 CC complementarity determining regions (CDRs). Phage display libraries were
 CC subjected to eight rounds of selection to isolate variants with an
 CC antigen binding affinity at least two-fold stronger than the binding
 CC affinity of parent antibody for the target VEGF antibody. The anti-VEGF
 CC antibody variants may be useful in diagnostic assays for detecting
 CC the prevention and treatment of neoplastic diseases such as breast
 CC cancer, lung cancer and retinoblastoma, and non-neoplastic diseases
 CC including rheumatoid arthritis, psoriasis, atherosclerosis, and diabetic
 CC and other proliferative retinopathies

XX SQ Sequence 118 AA;
 Query Match 100.0%; Score 655; DB 3; Length 118;
 Best Local Similarity 100.0%; Pred. No. 4.5e-55;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNGMNWVRQAPGKLEWVGWINTYTGSPY 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNGMNWVRQAPGKLEWVGWINTYTGSPY 60
 QY 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQGTLL 118
 DB 61 AADFKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQGTLL 118

RESULT 3
 AAB13381
 ID AAB13381 standard; protein; 118 AA.
 XX
 AC AAB13381;
 XX
 DT 12-SEP-2003 (revised)
 DT 21-NOV-2000 (first entry)
 XX
 DE F(ab)-12 anti-VEGF antibody heavy chain variable domain.
 XX
 KW Humanised; F(ab)-12; vascular endothelial cell growth factor; VEGF;
 KW antibody; antiinflammatory; cerebroprotective; cytostatic; antirheumatic;
 KW antiarthritic; antipruritic; antiarteriosclerotic; antidiabetic;
 KW antithyroid; excessive neovascularisation; tumour; rheumatoid arthritis;
 KW psoriasis; atherosclerosis; diabetes; retrolental fibroplasia;
 KW neovascular glaucoma; haemangioma; thyroid hyperplasia; Grave's disease;
 KW tissue transplantation; inflammation; oedema; trauma;
 KW complementarity determining region; CDR.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX
 PH Key Location/Qualifiers
 FT Region 26..35 /label= CDR-H1
 FT Region 50..66 /label= CDR-H2
 FT Region 70..79 /label= CDR-7
 FT Region 99..112 /label= CDR-H3
 XX
 PN WO200037502-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 09-DEC-1999; 99WO-US029475.
 XX
 PR 22-DEC-1998; 98US-00218481.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Van Bruggen N, Ferrara N;
 XX
 DR WPI; 2000-442646/38.
 XX
 PT Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis,
 PT diabetes and chronic inflammation in a mammal, comprises administering a
 PT human vascular endothelial cell growth factor antagonist.
 XX
 PS Disclosure; Fig 14B; 60pp; English.
 XX
 CC The present sequence is the heavy chain variable domain of humanised anti-
 CC -vascular endothelial cell growth factor (anti-VEGF) antibody F(ab)-12.
 CC It may be used to treat conditions characterised by undesirable excessive

CC neovascularisation. Such conditions include tumours (especially solid
 CC ones), rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and
 CC other retinopathies, retrolental fibroplasia, age-related macular
 CC degeneration, neovascular glaucoma, haemangiomas, thyroid hyperplasias
 CC (including Grave's disease), corneal and other tissue transplantation,
 CC and chronic inflammation. Oedemas associated with tumours, strokes and
 CC head trauma, and ascites associated with malignancies, meigs syndrome,
 CC lung inflammation, nephrotic syndrome, pericardial effusion and pleural
 CC effusion, may also be treated. Affinity matured anti-VEGF antibodies are
 CC also used as therapeutic agents. Monoclonal antibodies are generated in
 CC hybridoma cells and those with affinity for VEGF are identified by
 CC immunoprecipitation or by an in vitro binding assay. (Updated on 12-SEP-
 CC 2003 to standardise OS field)

XX Sequence 118 AA;

Query Match 100.0%; Score 655; DB 3; Length 118;
 Best Local Similarity 100.0%; Pred. No. 4.5e-55;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNGMNWVRQAPGKGLVWGWINTYTGPTY 60
 Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNGMNWVRQAPGKGLVWGWINTYTGPTY 60

Qy 61 AADPKRRFTSLDTSKSTAYLQNSLRADTAVYCAKYPHYGSSHWYFDVWGQGL 118
 Db 61 AADPKRRFTSLDTSKSTAYLQNSLRADTAVYCAKYPHYGSSHWYFDVWGQGL 118

RESULT 4

ID AAB13389 standard; protein; 118 AA.

AC AAB13389;

XX 21-NOV-2000 (first entry)

XX Anti-VEGF antibody Y0192 heavy chain variable domain.

XX Y0192; vascular endothelial cell growth factor; VEGF; antibody;
 KW antiinflammatory; cerebroprotective; cytotatic; antirheumatic;
 KW antiarthritic; antipsoriatic; antiarteriosclerotic; antidiabetic;
 KW antithyroid; excessive neovascularisation; tumour; rheumatoid arthritis;
 KW psoriasis; atherosclerosis; diabetes; retrolental fibroplasia;
 KW neovascular glaucoma; haemangioma; thyroid hyperplasia; Grave's disease;
 KW tissue transplantation; inflammation; oedema; trauma;
 KW complementarity determining region; CDR.

XX Unidentified.

Key	Region	Location/Qualifiers
FT	Region	26..35 /label= CDR-H1
FT	Region	50..66 /label= CDR-H2
FT	Region	70..79 /label= CDR-7
FT	Region	99..112 /label= CDR-H3

XX W0200037502-A2.

XX 29-JUN-2000.

XX 09-DEC-1999; 99WO-US029475.

XX 22-DEC-1998; 98US-00218481.

XX (GETH) GENENTECH INC.

XX Van Bruggen N, Ferrara N;

XX WPI; 2000-442646/38.

XX Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis,
 FT diabetes and chronic inflammation in a mammal, comprises administering a
 PT human vascular endothelial cell growth factor antagonist.

XX Disclosure; Fig 15B; 60pp; English.

XX The present sequence is the heavy chain variable region of the affinity
 CC matured anti-vascular endothelial cell growth factor (anti-VEGF) antibody
 CC Y0192. Humanised F(ab)-12 and affinity matured anti-VEGF antibodies may
 CC be used to treat conditions characterised by undesirable excessive
 CC neovascularisation. Such conditions include tumours (especially solid
 CC ones), rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and
 CC other retinopathies, retrolental fibroplasia, age-related macular
 CC degeneration, neovascular glaucoma, haemangiomas, thyroid hyperplasias
 CC (including Grave's disease), corneal and other tissue transplantation,
 CC and chronic inflammation. Oedemas associated with tumours, strokes and
 CC head trauma, and ascites associated with malignancies, meigs syndrome,
 CC lung inflammation, nephrotic syndrome, pericardial effusion and pleural
 CC effusion, may also be treated. Monoclonal antibodies are generated in
 CC hybridoma cells and those with affinity for VEGF are identified by
 CC immunoprecipitation or by an in vitro binding assay

XX Sequence 118 AA;

Query Match 100.0%; Score 655; DB 3; Length 118;
 Best Local Similarity 100.0%; Pred. No. 4.5e-55;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNGMNWVRQAPGKGLVWGWINTYTGPTY 60
 Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNGMNWVRQAPGKGLVWGWINTYTGPTY 60

Qy 61 AADPKRRFTSLDTSKSTAYLQNSLRADTAVYCAKYPHYGSSHWYFDVWGQGL 118

Db 61 AADPKRRFTSLDTSKSTAYLQNSLRADTAVYCAKYPHYGSSHWYFDVWGQGL 118

RESULT 5

ABP61247

ID ABP61247 standard; protein; 118 AA.

XX AC ABP61247;

XX 20-SEP-2002 (first entry)

XX Humanised anti-VEGF Y0101 antibody variable heavy domain.

XX Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
 KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
 KW retinal disorder; intraocular neovascular disorder; Y0101; heavy chain;
 KW variable domain.

XX Homo sapiens.

XX Mus sp.

XX Synthetic.

Key	Region	Location/Qualifiers
FT	Domain	26..35 /label= CDR-H1
FT	Domain	50..66 /label= CDR-H2
FT	Domain	70..79 /label= CDR-7
FT	Domain	99..112 /label= CDR-H3

XX US2002032315-A1.

XX 14-MAR-2002.

XX 06-APR-1998; 98US-00056160.

```

PR 06-AUG-1997; 97US-0054856P.
XX (BACA/) BACA M.
XX PA (WELL/) WELLS J A.
XX PA (PRES/) PRESTA L G.
XX PA (LOWM/) LOWMAN H B.
XX PA (CHEN/) CHEN Y M.
XX
XX PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
XX
XX DR WPI; 2002-517920/55.
XX
XX PT New humanized anti-VEGF (vascular endothelial growth factor) antibodies
XX PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
XX PT mammal, particularly for treating tumor or retinal disorders.
XX
XX PS Example 3; Fig 9; 47pp; English.
XX
XX CC The present invention relates to humanised anti-VEGF (vascular
XX CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
XX CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
XX CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
XX CC particularly those having a tumour or a retinal disorder e.g. intracocular
XX CC neovascular disorders. The present sequence is an exemplary heavy chain
XX CC variable domain of the humanised anti-VEGF antibody of the invention
XX
XX SQ Sequence 118 AA;
XX
XX Query Match 100.0%; Score 655; DB 5; Length 118;
XX Best Local Similarity 100.0%; Pred. No. 4.5e-55;
XX Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTNYGMNVRQAPGKGLVGVWNTYTGEPT 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTNYGMNVRQAPGKGLVGVWNTYTGEPT 60
OY 61 AADPKRRFTSLDTSKSTAYLQMNLSRAEDTAVYCAKYPHYGSSHWYFDVWGQGT 118
DB 61 AADPKRRFTSLDTSKSTAYLQMNLSRAEDTAVYCAKYPHYGSSHWYFDVWGQGT 118

RESULT 6
AAW70617
ID AAW70617 standard; peptide; 123 AA.
XX
XX AC AAW70617;
XX
XX DT 27-JAN-1999 (first entry)
XX
XX DE Anti-VEGF humanised antibody F(ab)-12 variable heavy domain.
XX
XX KW Heavy variable domain; murine; humanised antibody;
XX KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
XX KW VEGF-induced angiogenesis; tumour; retinal disorder;
XX KW age-related macular degeneration; diabetic retinopathy;
XX KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
XX
XX OS Synthetic.
XX OS Mus sp.
XX OS Homo sapiens.
XX
XX PN W09845331-A2.
XX
XX PD 15-OCT-1998.
XX
XX PF 03-APR-1998; 98WO-US006604.
XX
XX PR 07-APR-1997; 97US-00833504.
XX PR 06-AUG-1997; 97US-00908469.
XX
XX PA (GETH ) GENENTECH INC.
XX
XX PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

us-09-723-752b-7. rag
XX WPI; 1998-568337/48.
XX
XX PT New humanised antibody with affinity for vascular endothelial growth
XX PT factor - for treatment of tumours, retinal disease and other angiogenic
XX PT states, also related nucleic acid, vectors and transformed cells.
XX
XX PS Claim 7; Fig 1A; 100pp; English.
XX
XX CC The present sequence represents a variable heavy domain of the humanised
XX CC anti-vascular endothelial growth factor (anti-VEGF) antibody F(ab)-12.
XX CC The sequence is used to construct the humanised anti-VEGF antibody of the
XX CC invention. The humanised antibodies are used to inhibit VEGF-induced
XX CC angiogenesis, particularly for treating or preventing tumours (of any
XX CC type) and retinal disorders (e.g. age-related macular degeneration or
XX CC diabetic retinopathy). They can also be used to treat other conditions
XX CC that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,
XX CC atherosclerosis, Grave's disease, etc
XX
XX SQ Sequence 123 AA;
XX
XX Query Match 100.0%; Score 655; DB 2; Length 123;
XX Best Local Similarity 100.0%; Pred. No. 4.8e-55;
XX Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTNYGMNVRQAPGKGLVGVWNTYTGEPT 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTNYGMNVRQAPGKGLVGVWNTYTGEPT 60
OY 61 AADPKRRFTSLDTSKSTAYLQMNLSRAEDTAVYCAKYPHYGSSHWYFDVWGQGT 118
DB 61 AADPKRRFTSLDTSKSTAYLQMNLSRAEDTAVYCAKYPHYGSSHWYFDVWGQGT 118

RESULT 7
ABP61186
ID ABP61186 standard; protein; 123 AA.
XX
XX AC ABP61186;
XX
XX DT 20-SEP-2002 (first entry)
XX
XX DE Humanised anti-VEGF F(ab) (F(ab)-12) antibody variable heavy domain.
XX
XX KW Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
XX KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
XX KW retinal disorder; intracocular neovascular disorder; F(ab) (F(ab)-12);
XX KW heavy chain; variable domain.
XX
XX OS Homo sapiens.
XX OS Mus sp.
XX OS Synthetic.
XX
XX PN US2002032315-A1.
XX
XX PD 14-MAR-2002.
XX
XX PF 06-APR-1998; 98US-00056160.
XX
XX PR 06-AUG-1997; 97US-0054856P.
XX
XX PA (BACA/) BACA M.
XX PA (WELL/) WELLS J A.
XX PA (PRES/) PRESTA L G.
XX PA (LOWM/) LOWMAN H B.
XX PA (CHEN/) CHEN Y M.
XX
XX PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
XX
XX DR WPI; 2002-517920/55.
XX
XX PT New humanized anti-VEGF (vascular endothelial growth factor) antibodies
XX PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a

```

PT mammal, particularly for treating tumor or retinal disorders.

PS Claim 7; Fig 1; 47pp; English.

XX The present invention relates to humanised anti-VEGF (vascular
XX endothelial growth factor) antibodies or a variant of a parent anti-VEGF
XX antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
XX inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
XX particularly those having a tumour or a retinal disorder e.g. intraocular
XX neovascular disorders. The present sequence is an exemplary heavy chain
XX variable domain of the humanised anti-VEGF antibody of the invention

XX Sequence 123 AA;

Query Match 100.0%; Score 655; DB 5; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.8e-55;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFFTNYGMNVRQAPGKGLVWGWINTYTGEPY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFFTNYGMNVRQAPGKGLVWGWINTYTGEPY 60
QY 61 AADPKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQGL 118
DB 61 AADPKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQGL 118

RESULT 8

ADG31767
ID ADG31767 standard; protein; 123 AA.

XX AC ADG31767;

XX DT 26-FEB-2004 (first entry)

XX V(H) domain of parental humanised murine anti-VEGF antibody SeqID1.

XX protein library; in silico; VEGF; vascular endothelial growth factor;
XX antibody; computational prediction; V(H) domain; mouse; murine.

XX Synthetic.
XX Mus sp.

XX WO2003099999-A2.
XX 04-DEC-2003.

XX 20-MAY-2003; 2003WO-US016037.

XX 20-MAY-2002; 2002US-00153159.

XX 20-MAY-2002; 2002US-00153176.

XX (ABMA-) ABMAXIS INC.

XX Luo P, Hsieh M, Zhong P, Wang C, Cao Y, Liu S;

XX WPI; 2004-035117/03.

XX Constructing antibody libraries for generating protein libraries with
XX improved biological function comprising selecting from tester protein
XX sequences two peptide segments having 15% sequence identity with the lead
XX sequence.

XX Disclosure; SEQ ID NO 1; 354pp; English.

XX This invention relates to a novel method for the generation and screening
XX of a protein library in silico. Specifically, it refers to a high-
XX throughput method optimised for the identification of anti-VEGF (vascular
XX endothelial growth factor) antibodies with improved binding affinities
XX for their target antigen (VEGF), using computational prediction. The
XX present invention describes selecting proteins with a desirable function
XX based on their structural similarity to the target structural or
XX functional motif of a lead protein of interest. Accordingly, these

CC protein libraries are functionally biased with increased diversity so as
CC to increase the chance of identifying novel hits or combinations of
CC mutants with enhanced binding affinity. Furthermore, the sequence profile
CC based on the multiple structure alignment of the available lead structure
CC allows the sampling of a larger sequence space than by traditional,
CC multiple sequence alignment approaches. This polypeptide sequence is the
CC V(H) domain of parental humanised murine anti-VEGF antibody, used in an
CC exemplification of the invention.

XX Sequence 123 AA;

Query Match 100.0%; Score 655; DB 8; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.8e-55;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFFTNYGMNVRQAPGKGLVWGWINTYTGEPY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFFTNYGMNVRQAPGKGLVWGWINTYTGEPY 60
QY 61 AADPKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQGL 118
DB 61 AADPKRRFTSLDTSKSTAYLQMSLRADTAIVYCAKYPHYGSSHWYFDVWGQGL 118

RESULT 9

ADG31780
ID ADG31780 standard; protein; 123 AA.

XX AC ADG31780;

XX DT 26-FEB-2004 (first entry)

XX V(H) domain of the anti-VEGF two chain antibody AM2 protein SeqID 14.

XX protein library; in silico; VEGF; vascular endothelial growth factor;
XX antibody; computational prediction; V(H) domain; flexon; AM2;
XX two chain antibody; murine; mouse.

XX Synthetic.
XX Unidentified.

XX Mus sp.

XX WO2003099999-A2.

XX 04-DEC-2003.

XX 20-MAY-2003; 2003WO-US016037.

XX 20-MAY-2002; 2002US-00153159.

XX 20-MAY-2002; 2002US-00153176.

XX (ABMA-) ABMAXIS INC.

XX Luo P, Hsieh M, Zhong P, Wang C, Cao Y, Liu S;

XX WPI; 2004-035117/03.

XX Constructing antibody libraries for generating protein libraries with
XX improved biological function comprising selecting from tester protein
XX sequences two peptide segments having 15% sequence identity with the lead
XX sequence.

XX Disclosure; SEQ ID NO 14; 354pp; English.

XX This invention relates to a novel method for the generation and screening
XX of a protein library in silico. Specifically, it refers to a high-
XX throughput method optimised for the identification of anti-VEGF (vascular
XX endothelial growth factor) antibodies with improved binding affinities
XX for their target antigen (VEGF), using computational prediction. The
XX present invention describes selecting proteins with a desirable function
XX based on their structural similarity to the target structural or
XX functional motif of a lead protein of interest. Accordingly, these

CC protein libraries are functionally biased with increased diversity so as
 CC to increase the chance of identifying novel hits or combinations of
 CC mutants with enhanced binding affinity. Furthermore, the sequence profile
 CC based on the multiple structure alignment of the available lead structure
 CC allows the sampling of a larger sequence space than by traditional,
 CC multiple sequence alignment approaches. This polypeptide sequence is the
 CC V(H) domain of the anti-VEGF two chain antibody AMU protein, used in an
 CC exemplification of the invention.

XX Sequence 123 AA;

Query Match 100.0%; Score 655; DB 8; Length 123;
 Best Local Similarity 100.0%; Pred. No. 4.8e-55;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNYGMNVRQAPGKGLVWGWINTYTGEPT 60
 Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNYGMNVRQAPGKGLVWGWINTYTGEPT 60
 Qy 61 AADPKRRFTSLDTSKSTAYLQMNLSRAEDTAVYCAKYPHYGSSHWYFDVWGQGL 118
 Db 61 AADPKRRFTSLDTSKSTAYLQMNLSRAEDTAVYCAKYPHYGSSHWYFDVWGQGL 118

RESULT 10

ID ADC26155 standard; protein; 231 AA.

XX ADC26155;

DT 18-DEC-2003 (first entry)

XX Parent anti-VEGF Y0101 antibody wild-type heavy chain protein.

XX antibody variant; cytostatic; cancer; parent; anti-VEGF;
 KW vascular endothelial growth factor; Y0101; heavy chain; wild-type.

XX Unidentified.

XX WO2003068801-A2.

XX 21-AUG-2003.

XX 11-FEB-2003; 2003WO-US004184.

XX 11-FEB-2002; 2002US-035895P.

XX 10-SEP-2002; 2002US-0409685P.

XX (GETH) GENENTECH INC.

XX Lowman HB, Marvin JS;

XX WPI; 2003-697521/66.

XX Making an antibody variant of a parent antibody specific to an antigen by
 PT identifying a target amino acid residue within the variable domain of the
 PT parent antibody and substituting the target residue with a different
 PT amino acid residue.

XX Example 1; SEQ ID NO 2; 81pp; English.

XX The invention relates to a novel method for making an antibody variant of
 CC a parent antibody specific to an antigen. This is achieved via
 CC identifying a target amino acid residue within the variable domain of the
 CC parent antibody and substituting the target residue with a different
 CC replacement amino acid residue such that the charge complementarity
 CC between the antibody and antigen is increased. The antibody variant of
 CC the invention demonstrates cytostatic activity whilst the method may be
 CC useful for treating cancer. The current sequence is that of the parent
 CC anti-VEGF (vascular endothelial growth factor) Y0101 antibody Fab
 CC fragment heavy chain protein of the invention.

XX Sequence 231 AA;

Query Match 100.0%; Score 655; DB 7; Length 231;
 Best Local Similarity 100.0%; Pred. No. 9.6e-55;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNYGMNVRQAPGKGLVWGWINTYTGEPT 60
 Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNYGMNVRQAPGKGLVWGWINTYTGEPT 60

Qy 61 AADPKRRFTSLDTSKSTAYLQMNLSRAEDTAVYCAKYPHYGSSHWYFDVWGQGL 118
 Db 61 AADPKRRFTSLDTSKSTAYLQMNLSRAEDTAVYCAKYPHYGSSHWYFDVWGQGL 118

RESULT 11

ADQ90736 standard; protein; 476 AA.

XX ADQ90736;

XX 21-OCT-2004 (first entry)

XX Anti-VEGF antibody heavy chain protein SEQ ID NO:19.

XX antibody; antigen binding fragment; cell culture; variable domain;
 KW modified framework region; hypervariable region; cytostatic;
 KW antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
 KW tumour; inflammatory disorder; angiogenic disorder;
 KW immunological disorder; anti-VEGF antibody;
 KW anti vascular endothelial cell growth factor antibody; heavy chain.

XX Homo sapiens.

XX Synthetic.

XX WO2004065417-A2.

XX 05-AUG-2004.

XX 23-JAN-2004; 2004WO-US001844.

XX 23-JAN-2003; 2003US-0442484P.

XX (GETH) GENENTECH INC.

XX Simmons L;

XX WPI; 2004-562149/54.

XX N-PSDB; ADQ90720.

XX Producing an antibody or antigen binding fragment in high yield in a cell
 PT culture, comprises expressing a variable domain with a modified framework
 PT region in a host cell.

XX Example 6; SEQ ID NO 25; 161pp; English.

XX The present invention describes a method for producing an antibody or
 CC antigen binding fragment in high yield in a cell culture. The method
 CC comprises expressing a variable domain of the antibody or antigen binding
 CC fragment comprising a modified framework region (FR) in a host cell, and
 CC recovering the antibody or antigen binding fragment variable domain
 CC comprising the modified framework from the host cell. The modified FR in
 CC the method described above has a substitution of at least one amino acid
 CC position with a different amino acid, where the different amino acid is
 CC the amino acid found at the corresponding FR position of a human subgroup
 CC variable domain consensus sequence that has a hypervariable region 1
 CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
 CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
 CC The antibody or antigen binding fragment variable domain comprises the
 CC modified FR that has improved yield in cell culture compared to an
 CC unmodified antibody or antigen-binding fragment. The antibody and antigen
 CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and
 CC immunomodulatory activities, and can be used in antibody therapy. The
 CC methods and compositions of the present invention are useful for

producing antibodies or antigen binding fragments in cell culture, in particular for improving the yield of recombinant antibodies or antigen binding fragments in cell culture. The antibodies of the invention can be used to diagnose, treat, inhibit or prevent e.g. tumours and inflammatory, angiogenic and immunological disorders. The present sequence represents the heavy chain of an anti-VEGF (vascular endothelial cell growth factor) antibody, which is used in the exemplification of the present invention.

Query Match	100.0%;	Score 655;	DB 8;	Length 476;
Best Local Similarity	100.0%;	Pred. No. 2.2e-54;		
Matches 118;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	EVQLVPSG	GGGLVQPG	SGSLRLSC	AA	SYT	TNT	GMN	VR	QAP	KG	GLE	WGW	IN	TY	IG	STPY	60
Db	24	EVQLVPSG	GGGLVQPG	SGSLRLSC	AA	SYT	TNT	GMN	VR	QAP	KG	GLE	WGW	IN	TY	IG	STPY	83
Qy	61	AADF	KRRFT	PSL	DT	SK	STAY	LQ	NLS	RA	SD	TAV	Y	CA	KY	PH	YG	118
Db	84	AADF	KRRFT	PSL	DT	SK	STAY	LQ	NLS	RA	SD	TAV	Y	CA	KY	PH	YG	141

RESULT 12
AAW70680
ID AAW70680 standard; peptide; 118 AA.

DT	27-JAN-1999	(first entry)
XX		
XX		
DE		Anti-VEGF humanised antibody variable heavy domain of variant Y0192.
XX		
KW		Heavy variable domain; murine; humanised antibody;
KW		anti-vascular endothelial growth factor antibody; anti-VEGF antibody
KW		VEGF-induced angiogenesis; tumour; retinal disorder;
KW		age-related macular degeneration; diabetic retinopathy;
KW		rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
XX
PN WO9845331-A2.
XX
XX
PD 15-OCT-1998.

XX	Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
PI	
XX	WPI; 1998-568337/48.
XX	
DR	
XX	New humanised antibody with affinity for vascular endothelial growth
PT	factor - for treatment of tumours, retinal disease and other angiogenic
PT	states, also related nucleic acid, vectors and transformed cells.
PT	
XX	Example 3; Fig 9B; 100pp; English.
PS	

The present sequence represents a variable heavy domain of an affinity-matured anti-vascular endothelial growth factor (anti-VEGF) antibody variant. The sequence is used in the course of the invention to produce the humanised anti-VEGF antibody of the invention. The humanised antibodies are used to inhibit VEGF-induced angiogenesis, particularly for treating or preventing tumours (of any type) and retinal disorders (e.g. age-related macular degeneration or diabetic retinopathy). They can also be used to treat other conditions that involve angiogenesis, e.g.

CC rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc
XX
SQ Sequence 118 AA;

Query Match 99.4%; Score 651; DB 2; Length 118;
Best Local Similarity 99.2%; Pred. No. 1.le-54;
Matches 117; Conservative 1; Mismatches 0; Gaps 0;

Qy	1	EVOLVESGGGLVOPGGSGLRLSCAAAGSYFTNTYGNMWRQAPGKGLBWVGWINTYTGSPTY	60
Db	1	EVOLVESGGGLVOPGGSGLRLSCAAAGSYFTNTYGNMWRQAPGKGLBWVGWINTYTGSPTY	60
Qy	61	AADFKRPFSLDTSKSTAYLQNMNLSRAEDTAVYCAKYPHYGSSHWYFDVWGQGL	118
Db	61	AADFKRPFSLDTSKSTAYLQNMNLSRAEDTAVYCAKYPHYGSSHWYFDVWGQGL	118

RESULT 13
ABP61249
ID ABP61249 standard; protein; 118 AA.

AA	
DT	20-SEP-2002 (first entry)
XX	
DE	Humanised anti-VEGF Y0192 antibody variable heavy domain.

OS	Homo sapiens.
OS	Mus sp.
OS	Synthetic.

PH	Key	Location/Quali
FT	Domain	26. .35
FT	Domain	/label= CDR-H1
FT	Domain	50. .66
FT	Domain	/label= CDR-H2
FT	Domain	70. .79
FT	Domain	/label= CDR-7
FT	Domain	99. .112
FT	Domain	/label= CDR-H3

XX	US2002032315-A1.
PN	
XX	
XX	
PD	14-MAR-2002.
XX	
PF	06-APR-1998;
XX	98US-00056160.
PR	06-AUG-1997;
	97US-0054856P.

XX PA (BACA/) BACA M.
PA (WELL/) WELLS J A.
PA (PRES/) PRESTA L G.
PA (LOWM/) LOWMAN H B.
PA (CHEN/) CHEN Y M.

AA Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
PI
XX
DR WPI: 2002-517920/55.

New humanized anti-VEGF (vascular endothelial growth factor) antibodies or their variants, useful for inhibiting VEGF-induced angiogenesis in a mammal, particularly for treating tumor or retinal disorders.

CC The present invention relates to humanised anti-VEGF (vascular
CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
CC

CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
CC particularly those having a tumour or a retinal disorder e.g. intraocular
CC neovascular disorders. The present sequence is an exemplary heavy chain
CC variable domain of the humanised anti-VEGF antibody of the invention
XX
SQ Sequence 118 AA;

Query Match 99.4%; Score 651; DB 5; Length 118;
Best Local Similarity 99.2%; Pred. No. 1.1e-54;
Matches 117; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNGMNVRAQPGKGLVWGWINTYIGTEPT 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNGMNVRAQPGKGLVWGWINTYIGTEPT 60

QY 61 AADPKRRTFTSLDTSKSTAYLQMSLAEDTAVYCAKPHYGSSHWYFDVWGQGTLL 118
DB 61 AADPKRRTFTSLDTSKSTAYLQMSLAEDTAVYCAKPHYGSSHWYFDVWGQGTLL 118

RESULT 14

ADG31892
ID ADG31892 standard; peptide; 123 AA.

XX AC ADG31892;

XX DT 26-FEB-2004 (first entry)

XX DE V(H) protein sequence of anti-VEGF antibody X64 SeqID 126.

XX protein library; in silico; VEGF; vascular endothelial growth factor;
XX antibody; computational prediction; V(H) domain.

XX OS Unidentified.

XX PN WO2003099999-A2.

XX PD 04-DEC-2003.

XX PF 20-MAY-2003; 2003WO-US016037.

XX PR 20-MAY-2002; 2002US-00153159.

XX PR 20-MAY-2002; 2002US-00153176.

XX PA (ABMA-) ABMAXIS INC.

XX PI Luo P, Hsieh M, Zhong P, Wang C, Cao Y, Liu S;

XX WPI; 2004-035117/03.

XX Constructing antibody libraries for generating protein libraries with
XX improved biological function comprising selecting from tester protein
XX sequences two peptide segments having 15% sequence identity with the lead
XX sequence.

XX Disclosure; SEQ ID NO 126; 354pp; English.

XX This invention relates to a novel method for the generation and screening
XX of a protein library in silico. Specifically, it refers to a high-
XX throughput method optimised for the identification of anti-VEGF (vascular
XX endothelial growth factor) antibodies with improved binding affinities
XX for their target antigen (VEGF), using computational prediction. The
XX present invention describes selecting proteins with a desirable function
XX based on their structural similarity to the target structural or
XX functional motif of a lead protein of interest. Accordingly, these
XX protein libraries are functionally biased with increased diversity so as
XX to increase the chance of identifying novel hits or combinations of
XX mutants with enhanced binding affinity. Furthermore, the sequence profile
XX based on the multiple structure alignment of the available lead structure
XX allows the sampling of a larger sequence space than by traditional,
XX V(H) protein sequence alignment approaches. This polypeptide sequence is the
XX exemplification of the invention.

XX SQ Sequence 123 AA;

Query Match 99.2%; Score 650; DB 8; Length 123;
Best Local Similarity 99.2%; Pred. No. 1.4e-54;
Matches 117; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNGMNVRAQPGKGLVWGWINTYIGTEPT 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFITNGMNVRAQPGKGLVWGWINTYIGTEPT 60

QY 61 AADPKRRTFTSLDTSKSTAYLQMSLAEDTAVYCAKPHYGSSHWYFDVWGQGTLL 118
DB 61 AADPKRRTFTSLDTSKSTAYLQMSLAEDTAVYCAKPHYGSSHWYFDVWGQGTLL 118

RESULT 15

ADG31895
ID ADG31895 standard; peptide; 123 AA.

XX AC ADG31895;

XX DT 26-FEB-2004 (first entry)

XX DE V(H) protein sequence of anti-VEGF antibody D36 SeqID 129.

XX protein library; in silico; VEGF; vascular endothelial growth factor;
XX antibody; computational prediction; V(H) domain.

XX OS Unidentified.

XX PN WO2003099999-A2.

XX PD 04-DEC-2003.

XX PF 20-MAY-2003; 2003WO-US016037.

XX PR 20-MAY-2002; 2002US-00153159.

XX PR 20-MAY-2002; 2002US-00153176.

XX PA (ABMA-) ABMAXIS INC.

XX PI Luo P, Hsieh M, Zhong P, Wang C, Cao Y, Liu S;

XX WPI; 2004-035117/03.

XX Constructing antibody libraries for generating protein libraries with
XX improved biological function comprising selecting from tester protein
XX sequences two peptide segments having 15% sequence identity with the lead
XX sequence.

XX Disclosure; SEQ ID NO 129; 354pp; English.

XX This invention relates to a novel method for the generation and screening
XX of a protein library in silico. Specifically, it refers to a high-
XX throughput method optimised for the identification of anti-VEGF (vascular
XX endothelial growth factor) antibodies with improved binding affinities
XX for their target antigen (VEGF), using computational prediction. The
XX present invention describes selecting proteins with a desirable function
XX based on their structural similarity to the target structural or
XX functional motif of a lead protein of interest. Accordingly, these
XX protein libraries are functionally biased with increased diversity so as
XX to increase the chance of identifying novel hits or combinations of
XX mutants with enhanced binding affinity. Furthermore, the sequence profile
XX based on the multiple structure alignment of the available lead structure
XX allows the sampling of a larger sequence space than by traditional,
XX V(H) protein sequence alignment approaches. This polypeptide sequence is the
XX exemplification of the invention.

XX SQ Sequence 123 AA;

Query Match 99.1%; Score 649; DB 8; Length 123;

Best Local Similarity 98.3%; Pred. No. 1.8e-54;
Matches 116; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY	1	EVQLVESGGGLVQPGGSLRLS	CAASGYTFTNYGMNVRQAPGKGL	EWGMINITYTGEPTY	60
Db	1	EVQLVQSGGGLVQPGGSLRLS	CAASGYTFTNYGMNVRQAPGKGL	EWGMINITYTGEPTY	60
QY	61	AADEFKRRFTSLDTSKSTAYL	QNSLRADTAVYICAKYPHYGSS	HWYFDVWGQGTLL	118
Db	61	AADEFKRRFTSLDTSKSTAYL	QNSLRADTAVYICAKYPHYGSS	HWYFDVWGQGTLL	118

Search completed: March 14, 2005, 20:39:15
Job time : 95.4518 secs

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ **BLACK BORDERS**
- ☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- ☐ **FADED TEXT OR DRAWING**
- ☐ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- ☐ **SKEWED/SLANTED IMAGES**
- ☐ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- ☐ **GRAY SCALE DOCUMENTS**
- ☐ **LINES OR MARKS ON ORIGINAL DOCUMENT**
- ☐ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- ☐ **OTHER:** _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.